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JOURNAL
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COMMENT
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CG613923/c
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Search completed: March
Job time: 2947 secs
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Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
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E 1 (bases 1 to 68)

S Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Finch,R.A., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Priddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Rey,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Spayne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Shu,Q., Person,C. and Sands,A.T.
Zhu,Q., Person,C. and Sands,A.T.
What kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention L. Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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CG613923 CG613923.1 GI:37437772
GSS.
                                                                                                                                   1 ATAAAAAGCTTCTTC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse E:
described in Zambrowicz et al (Nature. 1998 Apr 9;392(66'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14610273
Contact: Zambrowicz BP
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                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10000"
/clone="0ST301723"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
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Pred. No. 1.3e+05;
0; Mismatches 1;
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1998 Apr 9;392(6676):608-11)
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AG222033/c
                                       FEATURES
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                                                Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/, Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                                                                                                          Sato, S., Nakamura, Y. and Tabata, S. Lotus japonicus BAC End sequences Published Only in Database (2002) 2 (bases 1 to 65)
                                                                                                                                                                                                                                                                           Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons;
Cornids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                         Direct Submission
                                                                                                                                                             Sato, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                       survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Horticulture and Food Research Institute of New Zealand Mt Albert Rd, Mt Albert, Auckland, New Zealand: 00 64 09 815 4200; 00 64 09 815 4201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    est@hortresearch.co.nz.
 organism="Lotus corniculatus var. japonicus"
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Research & Development"
                                  Location/Qualifiers
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/clone_lib="(AAAA) Royal Gala 59 DAFB
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db_xref="taxon:3750"
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Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: McCarter JP
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Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu)
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Waller, T., Berney, C., Waller, T., Waller, Waller, T., Waller, Waller,
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Heterodera glycines cDNA 5', ml
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The vector to vector length is 68.
Location/Qualifiers
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The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 67)
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
                               /note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes are the OP25 strain. Frozen J2 nematodes were provided by Dr. Rick Pavis of Parents of Strain.
Davis of North Carolina State University"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:51029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="LjB06h23_r"
/clone_lib="genomic BAC library"
/note="VECTOR:pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="Miyakojima MG-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dev_stage="enriched for 2nd stage juveniles"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Heterodera glycines'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:34305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _lib="Heterodera glycines J2 pAMP1 v8 Chiapelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 10
Pred. No. 1.3e+05;
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RESULT 25
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Marrin,J.,
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Materston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM094204.1 GI:17023170
EST.
Glycine max (soybean)
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Putative full length read vector to vector length is 79 This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 US (phone: 800 423 4163; email: info@biogeneticservices.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sah26f06.y1 Gm-c1036 Glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1036-2579 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM094204
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
/clone lib="Gm-cl036"
/clone lib-"Gm-cl036"
/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; This
/note="Vector: pSPORT1 year from mRNA isolated from
somatic embryos (age ranging from 2 months to 9 months)
cultured on MSD 20. The library was prepared using the
Life Technologies pSuperScript cDNA library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a Not1 restrictions site. Sal1
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by Not1 digestion. The cDNA fragments
were directionally cloned into the Not1-Sal1 restriction
site of the pSPORT1 vector. The ligated cDNA fragments
were transformed into E.coli ElectroMax DH10B host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          est@watson.wustl.edu
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/db_xref="taxon:10090"
/clone="MHPP302k23"
/clone_lib="MHPP"
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                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1036-2579"
/tissue_type="somatic embryos cultured on MSD 20"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                        Locus
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DEFINITION

CN855909 000721AAAA003533HT (AAAA)

64 bp Royal

Gala

mRNA linear La 59 DAFB fruit,

EST 03-JUN-2004

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RESULT 26
BF718349/c
LOCUS
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ORGANISM
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VERSION
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RESULT 27
                                                                                                                          Query Match
Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dermatology Branch
National Cancer Institute
Building 10, Room 12N238,
20892-1908, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 59)

Darling,T.N., Koh,B.B and Yancey,K.B.

Delineation of Genes Expressed in Human

Sequencing of a CDNA Library from Laser

J. Invest Dermatcl. 112 (4), 673 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST122 microdissected normal human epiclone S81230.NIH-39 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF718349.1 GI:12017448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF718349
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                                                                                          2 TAAAAAGCTTCTTCA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 59.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 402 1863
Fax: 301 496 5370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yancey, K.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer: M13R
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                                                                                                                              Conservative
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                                                                                                                                                                                                                                  /clone lib="microdissected normal human epidermis"
/note="Organ: skin; Vector: pAMP1; Epidermis from 20
cryostat skin sections (8 um thick) was selectively
isolated using laser capture microdissection. Total RNA
was extracted, reverse transcribed, and directionally
cloned using uracyl DNA glycosylase (Krizman protocol 2
see http://www.ncbi.nlm.nih.gov/
                                                                                                                                                                                                                CGAP/info/libconst.cgi#Protocol2)."
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="epidermis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                            clone="S81230.NIH-39"
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93.3%;
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                                                                                                                            Score 13.4; D
Pred. No. 1.2e
0; Mismatches
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                                                                                                                              DB 2;
L.2e+05;
hes 1;
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Capture Microdissected Skin
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REFERENCE
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BH865173
LOCUS
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KEYWORDS
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                                      Query Match
Best Local Similarity
Matches 16; Conserv
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1 ATAAAAAGCTTCTTCAACAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 bp DNA linear GSS 05-AUG-200 SALK 097512 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_097512, genomic survey server BH865173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R. A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _
                                                                                                                                                                                                                                                                                                                                                                                                                 Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH865173.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ecker@salk.edu
                                                                                                                            /db xref="taxon:3702"
/clone="SALK 097512"
/clone="Ib="Arabidopsis thaliana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sub_species="morsitans"
/db_xref="raxon:37546"
/clone="Tsell9902_q1c"
/tissue_type="adult infected gu/clone_lib="Glossina morsitans
                                                                                                                                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Glossina morsitans morsitans"
|mol_type="mRNA"
|mol_type="mRNA"
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                                                         68.0%;
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                                                         Score 13.6;
Pred. No. 1
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Pred. No. 9.7e+04;
                                      Mismatches
                                                    1e+05;
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                                                                       Length 68;
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              Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                               1 (bases 1 to 77)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G.,
                                                                                                                                                                                                                                                 GSS; genome survey sequence; MICER. Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                         chromosome engineering CR103372 CR103372.1 GI:49850772
                                                                                                                                                                                                                                                                                                                             CR103372 77 bp DNA linear GSS 05-JUI Reverse strand read from insert in 3'HPRT insertion targeting Chromosome engineering clone MHPP302k23, genomic survey sequer
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AV560198
thaliana
                                                                                                                                                         Mammalia; Eutheria; Euarchontoglires; Glires;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                               Direct Submission
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                 Rogers, J. and Bradley, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10907847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 76)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV560198.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 bp mRNA linear EST 23-FEB-20 Arabidopsis thaliana green siliques Columbia Arabidopsis CDNA clone SQ130h07F 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="green siliques"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="SQ130h07F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.6; DB Pred. No. 1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                    van der Weyden,
Nishijima, I., Y
                                          Cambridgeshire,
                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                          GSS 05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 23-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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db\_xref="taxon:10090" /strain="C57BL/6J"

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RESULT 20
DN252834/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                              Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q., Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R., Maguire, L., Kennedy, S., Waterston, R. and Wilson, R. WashU Hydra EST Project Unpublished (2002)
On Mar 1, 2005 this sequence version replaced gi:60415302.
Contact: Hans Bode WashIngton University School of Medicine WashIngton University School of Medicine WashIngton University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATAAAAAGCTTCTTCAACAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydra magnipəpillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAB-aab71i16.gl Hydra UCI6-
cDNA 5', mPNA accession
                                                                                             Library material provided by Hans Bode & Dirk Lindgens, Univ. of Calif., Irvine Library constructed by Dirk Lindgens, Univ. of Calif. Irvine Library sequenced by Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)

This trace has been recalled with phred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DN252834.2 GI:68378215
original value before phred recall for SL was 104 original value before phred recall for SR was 392 Seg primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 52)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and with adaptors complementary to the insert adaptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory Mouse DNA Resource
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Pred. No. 9.5e+04;
0; Mismatches 4;
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barcoded EST's
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s Hydra magnipapillata
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8 밁

ORIGIN

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RESULT 21
BX551631
LOCUS
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AUTHORS
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VERSION
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PUBMED
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Best Local
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATAAAAAGCTTCTTCAACAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                            Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX551631 54 bp mRNA linear E BX551631 Glossina morsitans morsitans adult infected
                        All clones with suffix qlc are reverse primer reads starting end of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                         Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                            Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 4 (10), R63 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glossina morsitans morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX551631.1 GI:33375953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              morsitans morsitans cDNA clone Tsell9g02_q1c, mRNA sequence
                                                                                                                                                                                                                                                                                                                    Contact: Hall N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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b. Double-stranded cDNA was ligated to Sal I adapter,
digested with NotI and cloned into the pSPORTI vector
pre-cut with NotI and Sall. c. The ligation mix was
transformed into DH10B cells. d. The cells were grown in
SCC=5g yeast, 20g tryptone, 0.5g NaCl, 10mM MgSO4, 10mM
MgCl, 0.2% glucose/liter, (no antibiotic) e. DMSO was
added to a final conc. of 10% as a cryoprotectant and
frozen. f. The titre before freezing was determined as
1500/100ul. Assuming a 10% loss upon freezing, the titre
is probably ~ 13500clones/ul g. 3 tubes each containing ~
13500 clones/ul [=total of ~40,500] are enclosed. h. The
frequency of vectors containing inserts is 90% as
determined by digestion check after picking 20 clone,
miniprep and subsequent digestions with NotI and Sal I. i.
A low level of 32P was used in the CDNA synthesis
procedure. The level measured by holding a Geiger Counter
next to a tube was background."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/note="Vector: pSPORT1; Site 1: Not I; Site_2: Sal I; a.
1st strand cDNA was primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hydra magnipapillata"
/mol_type="mRNA"
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Location/Qualifiers
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80.0%;

 Mismatches

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Pred. No. 9.6e+04;
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d gut Glossina
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FEATURES

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                                                                                                                                                  Gracey, A.Y., Fraser, E.J., Li, W., Fang, Y., Taylor, R.R., Rogers, J., Brass, A. and Cossins, A.R.
Coping with cold: An integrative, multitissue analysis of the transcriptome of a poikilothermic vertebrate
Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
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Nat. Gene
14981521
                          On Jan 3, 2003 this sequence version replaced gi:27490659. Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.

1 (bases 1 to 42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CcLL02a07o15f1 Carp liver library 2 Cyprinus carpio 07o15 5', mRNA sequence. CA964102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                      Cyprinus carpio
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA964102.2 GI:50737080
  School of Biological Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                        Cyprinus carpio (common carp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target recognition sequence. Class: transposon insertion site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    piggyBac element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence recovery method was inverse PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Roger A Hoskins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This insertion position refers to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The piggyBac insertion position is unspecified in the 40 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAAAGTTTCTTTAACCC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAAAAAGCTTCTTCAACAC 20
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510 486 6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib=Excellxis piggyBac WH insertions"
/clone="Vector: piggyBac WH (GenBank accession number
/note="Vector: piggyBac WH (GenBank accession number
AY515148); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the WH element using the
constitutive alpha-1 tubulin:piggyBac transposase source.
We remobilized the WH element from a single ammunition
element on the Binsinecy balancer chromosome in dysgenic
females. We outcrossed dysgenic virgin females in vials to
the isogenic w- strain and selected new hops in the
following generation. All lines were mapped to a
chromosome by standard genetic methods, examined for
homozygous viability, and used for recovery of flanking
genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P and piggyBac
Genet. 36 (3), :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic_w-strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:7227"
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.6; DB 10;
Pred. No. 9.1e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
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The Biosciences Building, Crown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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Best Local :
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                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0047 row: F column: 07
                                                                                                                                                                                                                             University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud, Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 49)
                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATAAAAGCTTCTTCAACAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                               plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone UUGC2M0047F07 R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ794039
49 bp DNA linear GSS 16-FEB-200200047F07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                            Class: plasmid ends
                                                                                            Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Plate: 07 row: o column: 15

Seq primer: TriplEx 5' LD (5'-CTCGGGAAGCGCGCCATTGTGTTGGT-3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cossins@liv.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Street, Liverpool, United Kingdom, L69 7ZB Tel: +44(0)151-795-4510 Fax: +44(0)151-795-4431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAAAAGTGTGTTCAACTC 23
                                                                                                                                                                                                   908,
308,
USA
                                    quality sequence stop: 49.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Liver"
/dev_stage="Adult"
/lab_host="E_coli Electromax DH10B"
/clone_lib="Carp_liver_library_2"
/clone_lib="Carp_liver_library_2"
/note="Vector: pTriplEx2; Site_1: Sfil GGCCATTACGGCC;
Site_2: Sfil GGCCGCCTCGGCC; Normalized and serially
subtracted cDNA library prepared from liver of warm, cold
and hypoxia challenged animals"
organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/mol type="mRNA"
/db xref="taxon:7962"
/clone="07o15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male & female"
                      . 49
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                                                                                                                                                                                                                                                                                       Weiss
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Pred. No. 9.
                                                                                                                                  Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
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RESULT 16
BX558717/c
LOCUS
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T74169/c
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PUBMED
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                 Local Similarity
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Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Farsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thiery-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
                                                                                                                                                                                              28
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T74169
T74169
TRNA linear EST 02-MAR-1995
YC60a12.sl Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE: 85054 3' similar to gb: A06977 SERUM ALBUMIN PRECURSOR
                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
                 BX558717 Glossina morsitans morsitans adult infected gut Glossina morsitans adult infected gut Glossina morsitans cDNA clone Tse3d01_q1c, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LLML This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 58 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4444 Forest Park Parkway, Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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T74169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Size: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domo sapiens (human)
  morsitans morsitans cDNA clone
BX558717
                                                                                                                                                                                                                                           TAAAAAGCTTCTTCAAC 18
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Location/Qualifiers
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
/clone lib="Stratagene liver (#937224)"
/note="Organ: liver; Vector: pBluescript SK; Site_1:
BCORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Cligo dT. Hepatectomy from normal male caucasian. Average
insert size: 1.1 kb; Uni-ZAP XR Vector; ~5' adaptor
sequence: 5' GAATTCGGCACCAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GDB:502111"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="IMAGE:85054"
                                                                                                                                                                                                                                                                                                              69.0%;
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                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 8;
Pred. No. 8.5e+04;
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                          DB
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SOURCE
ORGANISM
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DEFINITION
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CZ487745
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ORGANISM
                                                                                                                                                                                       REFERENCE
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PUBMED
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         TITLE
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

CE 1 (bases 1 to 40)

Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,

Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,

Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,

Ryner,L., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,

Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.

A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   School of Biological Sciences,
University of Wales,
Bangor LL57 20W
All clones with sweet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glossina morsitans morsitans Glossina morsitans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BX558717.1 GI:33365662
EST:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
                                                                                                                                                                                                                                                                                                                                                                                        CZ487745 40 bp DNA linear GSS 29-APR-2 f05125-5prime Exelixis piggyBac WH insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        All clones with suffix qlc are reverse end of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Biol. 4 (10), R63 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Hall N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14519198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response genes
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GSS.
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T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone Tib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Tse3d01_q1c"
/tissue_type="adult infected gut"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:37546"
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Pred. No. 9e
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AUTHORS
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CG511973
LOCUS
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Best Local S
Matches 15
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PUBMED
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Best Local (
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     46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, B.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Eayne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Shu, Q., Person, C. and Sands, A.T.
What in the second Sands, A.T.
White second Sands, A.T.
Whit
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OST64653 Mus musculus 129Sv/Ev NmRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lexicon Genetics Incorporated 4000 Research Forest Drive, The Woodlands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OmniBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Zambrowicz BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14610273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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CG511973.1
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                                                                                                                                           Similarity
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  ANNGAAAGCATCTTCAACA
                                                          ATAAAAAGCTTCTTCAACA 19
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                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                    /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="OST64653"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocat
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left border"
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/mol_type="genomic DNA"
/db xref="taxon:3702"
/clone="409A08"
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/ecotype="Wassilewskija"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 65
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                                                                                                                                           69.0%;
78.9%;
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  64
                                                                                                                                           Score 13.8; DB 10
Pred. No. 8.1e+04;
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                                                                                                                    Mismatches
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                                                                                                                                                                     DB 10;
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                                                                                                                 4;
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1998 Apr 9;392(6676):608-11)
                                                                                                                                                                   Length
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s cDNA clone
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                                                                                                              0
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CR358067
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29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-NNA. It indicates an insertion close to or within gene At3912400. Details on the protocols used for generation of the sequence are Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High-throughput generation of sequence mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosso, M.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strizhov, N., Li, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flanking sequence tag-based reverse Plant Mol. Biol. 53 (1-2), 247-259 (
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                                                                                     Conservative
                                                                                                                                                                                                                                                                             /ecotype="Col-0"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGABI1 (GenBank accession number: AY529716). The
                                                                                                                                                                                          lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                    /clone="GK-724C11-025362"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                                                                                                       Score 13.8; DB 11
Pred. No. 8.1e+04;
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Tanorh: 10000 Std Error: 0.00
                                                          Vitis vinifera var. Chardonnay Unpublished (2002) Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitiseae; Vitis.

1 (bases 1 to 56)
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Department of Biochemistry
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Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C5_BL/6J_(male)_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtai
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                  Submitted (23 OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
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GSS; left border; T-DNA flanking s
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Arabidopsis thaliana T-DNA flanking
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Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                            Balzergue, S.
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12446565
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/clone_lib="An expressed sequence tag database for abiotic
/clone_lib="in expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: XhoI"
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/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVC054A09"
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Pred. No. 7.8e+04;
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Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Harrouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. A. complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                    genomic survey sequence. CZ468098
                                                                                                                                                                                                                                                                                                                                              melanogaster genomic Sequence recovered from 5' end of genomic survivor commons.
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c02650-5prime Exelixis piggyBac PB insertions
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                                                                                                                                    1 (bases 1 to 37)
Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                  CZ468098
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BJ063523 NIBB Mochii normalized Xenopus tailb
laevis cDNA clone XL076120 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                    CZ468098.1 GI:62962111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed genes in X. laevis embryo Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://xenopus.nibb.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kitayama, A., Terasaka, C., Mochii, M., Ueno, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 32)
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81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tshini@genes.nig.ac.jp
formation of this clone is available through the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL076i20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Xenopus laevis"
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                      of piggyBac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 29-SEP-2003
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  JOURNAL
COMMENT
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PUBMED
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Best Local :
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AZ407584.1
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                                                                                                                                                                                                                                   Mus musculus
                                        plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14981521
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ407584 39 bp DNA linear GSS 0: 1M0178A15F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGC1M0178A15 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATAAAAAGCTTCTTCAA 17
                                                                               Mouse whole genome scaffolding with paired end
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The piggyBac insertion position is 34 in the insertion position refers to the first base crarget recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence orientation is forward piggyBac element.
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Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: transposon insertion site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Roger A Hoskins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAAAAACCTTCTTTAA 37
                                                                                                                                                                                                                           (bases 1 to 39)
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Genet. 36 (3), :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Exelixis piggyBac PB insertions"
/note="Vector: piggyBac PB (GenBank accession number / Note="Vector: piggyBac PB (GenBank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 370C water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
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/strain="isogenic w- strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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88.2%;
B. Weiss
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Pred. No. 7.
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of the 4 base
                                                                                  reads from 10kb
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RESULT 6
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AZ628248.1 GI:11750438
GSS. Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ628248 76 bp DNA linear GSS 13-DEC-20 1M0480D16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Clone UUGCIM0480D16 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0480 row: D column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ass: plasmid ends
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                     http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwn42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: pMp42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="UUGC1M0480D16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
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84.2%;
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Pred. No. 5.4e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed sequence tags
Theor. Appl. Genet. 108 (5), 903-913 (2004)
14624337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tian,A.G., Wang,J., Cui,P., Han,Y.J., Xu,H., Cong,L.J., Huang,X.G., Wang,X.L., Jiao,Y.Z., Wang,B.J., Wang,Y.J., Zhang,J.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max (soybean)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute of Genetics and Developmental Biology, CAS, China Datun road, Beijing 100101, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Characterization of soybean genomic features by analysis of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD395443.1 GI:31310240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq primer: T7 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 86-10-64886859
Fax: 86-10-64873428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Biotechnology Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chen S-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen
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AAAAGCTTCTTCAA 17
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                                                             Conservative
                                                                                                                                                                                                            /tisue_type="Geedlings"
/dev_stage="two-week seedlings"
/lab host="XL1-Blue MRF' strain"
/clone_lib="Soybean induced by Salicylic Acid"
/clone_lib="Soybean induced by Salicylic Acid"
/clone_lib="Soybean induced by Salicylic Acid"
/note="Wector: pBluescript SK+; Site_1: EcoR I; Site_2:
/note="Wector: pBluescript K+; Site_1: EcoR I; Site_2:
/note="Wector: pBluescript K+; Site_1: EcoR I; Site_2:
/note="Wector: pBluescript Site_2: EcoR I; Site_2:
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cultivar="Kefeng 1"
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84.2%;
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100.0%;
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                                                                                                   Score 14; DB 6; L; Pred. No. 6.8e+04;
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Pred. No. 5.4e+04;
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by Salicylic Acid Glycine max cDNA 3',
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                                                                                                                                 Length 80;
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Staten, N.R.
Direct Submission (/
Direct Submission (/
Direct Submission (/
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                                                                                                                                                                                                                                                                                                                                                                                                                        Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                      High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T89907

57 bp mRNA linear EST 20-M yellb09.rl Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117401 5' similar to gb:L11566 60S RIBOSOMAL PROTEIN L
                                                                                Seq primer: M13RP1
High quality seque
                                                                                                                     Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Lennon, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nick Staten
Tel: 636 247 6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: nicholas.r.staten@pfizer.com.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMAN);, mRNA sequence.
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                                                                              quality sequence stop: 1.
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/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1;
normal, untreated canine liver"
/organism="Homo sapiens"
/mol_type="mRNA"
                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
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84.2%;
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Pred. No. 5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                       St. Louis,
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                                                                                                                                                                                                                                    PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJ600260.1 GI:37949888
GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO Rep. 3 (12), 1152-1157 (2002) 12446565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brunaud, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ600260 75 bp I
Arabidopsis thaliana T-DNA flanking
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/lab_host="SOLR cells (kanamycin resistant)"
/clone lib="Stratagene lung (#937210)"
/note="Organ: lung; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhOI; Cloned unidirectionally. Primer:
Oligo dT. normal lung. Average insect size: 1.0 kb;
Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
right border"
                    /note="T-DNA flanking sequence
                                                                      /ecotype="Wassilewskija"
                                                                                                                                         db_xref="taxon:3702"
                                                                                                                                                                                           organism="Arabidopsis thaliana"
                                                                                            clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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/db_xref="taxon:9606"
/clone="IMAGE:117401"
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84.2%;
                                                                                                                                                                       _type="genomic DNA"
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Pred. No. 5.1e+04;
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AU009985
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AZ435382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished Contact: Mitsuoki Morimyo
Contact: Mitsuoki Morimyo
Genome Research Group
Genome Research Group
National Institute of Radiological Sciences
National Institute of Inage-ku, Chiba, Chiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU009985
AU009985 Schizosaccharomyces
Schizosaccharomyces pombe cDN
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 72)
Morimyo, M. and Mita, K.
Identification of expressed
                                                                                                            AZ435382
AZ435382.1
                                                                                                                                    AZ435382
47 bp DNA line
1M0222D23F Mouse 10kb plasmid UUGC1M library Mu
clone UUGC1M0222D23 F, genomic survey sequence.
                                                                                                                                                                                                                                                                           ,..
                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae;
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AU009985.1 GI:3346665
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63.0
63.0
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: Mi3mpl9; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the Smal site of Mi3mpl9 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="taxon:4896"
'clone="spc00766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="h minus"
                                                                                                             GI:10559395
                                                                                                                                                                                                                                                                                                                    72.0%;
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CB227096
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BX894115
                                                                                                                                                                                                                                                                                                                     Score 14.4; DB 1;
Pred. No. 4.3e+04;
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CA330935 haa94h05.
CB227096 1Ru34D11
CZ551924 CB2 393 C
BX894115 Arabidops
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                                                                                                                                                        genomic
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                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0222 row: D column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                              1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                           Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                               DN336224

LIB3187-017-P1-K1-G5 LIB3187

CLN1579719, mRNA sequence.

DN336224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                     EST
                                                                                                   DN336224.1
                                                                      Canis familiaris (dog)
                                                                                                                                                                                                                                                                                                           Similarity
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igh quality sequence stop: 47.
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801 585 7177
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="UUGC1M0222D23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="Male"
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                                                                                                    GI:60508916
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Pred. No. 4.9e+04;
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Canis
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C. Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10k Nouse whole genome scaffolding with paired end reads
                                                                                                                                                                                                    was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                     adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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AJ600260 Arabidops
AZ628248 1M0480D16
CD395443 Gm ck1546
BJ063523 BJ063523
CZ468098 CJ2650-59
AZ407584 1M0178A1-55
CD013073 VVC054A09
AJ594977 Arabidops
CG511973 OST64653
CR358067 Arabidops
CR358067 Arabidops
T74169 yc60a12.sl
BX558717 BX558717
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CF269390
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CV582865
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CD906653
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CD914664
AA1123303
AV852693
CZ194654
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CZ
CN855909 000721AAA
AG222033 LOCUS COT
BIT/49485 FO78f09 CY
EG613923 OST301723
BX94794 Arabidops
CD409537 Gm Cx3662
AA128473 z1Z4b03.x
AA615668 VO78902.r
CC888526 SALK 1521
CZ485190 FO2651-5p
CA340051 NISC 1910
D18199 MUSGS070469
AA515833 MISCOC12A06
BH904156 SALK 1521
CC72689390 FCY1C0145
AZ777832 ZM0012A08
AJ594453 Arabidops
CD906881 G468.1052
CY582865 L AM-aaaa2
CL521961 DAJ77004 F
CD906881 G468.1052
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CL521961 DAJ7704 F
CD906881 G468.1052
CY582761 L AM-aaa2
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CD906881 G468.1052
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CC5219654 BY003358
CD906882 G468.1052
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CC5219654 BY03357-N
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CC119667 BY006670
CC4270358 CO59761
CX471364 DV3305.r
BH005389 100806670
CC4270358 CO59761
CX471534 ON0530AY
CC119657 DALC1--02-
CB165090 1411 AN512044
CC2194564 DOS30AY
CC119456 DOS30AY
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CC317534 ON05250A4
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BH758136 SALK 0356
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AZ67937 TOVWATC1
BH005589 DOS3068
AZ694935 TOVWATC1
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AZ694935 TOVWATC1
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AZ694935 ANABIOD98
BH009975 SALK 0368
AZ139394 DALS93964
BH558869 G03383039
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Search completed: March Job time: 341.667 secs
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                                                                                                                                                                                                                                                                       CC A novel composition has been produced which comprises a bivalent CC polypeptide having an amino acid residue sequence of formula: V - V CC where V = an antigen binding site; X = an amino acid residue sequence of 5 to 120 amino acid residues. The present sequence represents the PCR CC primer BCl used in the preparation of anti-CD3 monospecific tetravalent cantigen-binding polypeptide. The polypeptides can assume a conformation having a binding site specific for a preselected or predetermined ligand such as an antigen, hapten or enzymatic substrate. They can be used in diagnostic assays and also for prophylactic or therapeutic applications. The bivalent antibodies can also be used for activating and crosslinking T cells in vitro or in vivo. The polypeptides exist in stable conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations and bind to target molecules with high avidity while conformations are provided functional molecules which can circulate in the body for longer periods of time than their Fab counterparts
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Matches 15
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                                                                                                                                                                                                                                      Sequence 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multi-specific and multi-valent ligand binding polypeptide(s) - comprise one or more antigen binding sites, for use in diagnostic, prophylactic and therapeutic methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multispecific; multivalent; ligand binding polypeptide; prophylactic; antigen binding site; hapten; enzyme; bivalent antibody; T cell; polymerase chain reaction; PCR; ss.
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Pred. No. 8.3e+03;
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                          The invention relates to novel Mowgli G-protein coupled receptor (GPCR) polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids, probes, antibodies, expression vectors and ligands are useful as biosensors, for detection, diagnosis, or treatment of diseases associated with over-, under- or abnormal expression of Mowgli GPCR in tissues, in genetic analysis and in chromosome identification. Polypeptides of the invention may be used for screening compounds which bind the receptor and which activate (agonists) or inhibit (antagonist) activation of Mowgli. They may further be used as vaccines to induce immunological response to produce antibody and/or T cell immune response against e.g. bacterial, protozoan, fungal or viral infections, pain, cancers, diabetes, obesity, anorexia, asthma, Parkinson's disease and other neurological disorders. The present sequence is human Mowgli G-protein coupled receptor DNA camplifying PCR primer used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33
                                                                                                                                                                                                                                                                                                                       New Mowgli G-protein coupled receptor polypeptides and polynucleotides, useful for inducing immunological response to produce antibody and/or {\tt T} cell immune response against e.g. bacterial, fungal, protozoan or viral
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-129261/12.
                                                                                                                                                                                                                                                                                                                                                                                                                        Carlton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Mowgli
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in; diabetes; vaccine; human; PCR; prime;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Dixon J,
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                         ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer;
                                                                                                                                                                                                                                                                                                                                                                                                                           Zahn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                           U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asthma; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #2
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Query

Sequence

42

B₽;

13

A; 5 C; 7

G; 17 Score

Η,

0 Other;

72

.0%;

14.4; 0 U;

DB

8

Length

42;

RESULT 30 AAT58883/c

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30

15

0

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RESULT 29
ABS55373/c
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                                                                                                                                                                                 CC capacity for controlling DNA damage-responding gene expression of a capacity for controlling DNA damage-responding gene expression of a CC promoter, and an expression cassette for a plant. The invention describes are expression cassette for a plant for expressing an exotic gene, by responding to DNA damage containing the above promoter and a site for inserting an exotic gene, so that said exotic gene is linked to said promoter expressably. Also described is a recombinant plasmid for promoter expressably. Also described is a recombinant plasmid for expressing an exotic gene by responding to DNA damage containing the above promoter and an exotic gene linked expressably to said promoter, a concept of the expression responding to DNA damage is desired including a step of transformed plant cell, and a transformed plant cell prepared by the containing a plant cell, and a transformed plant cell transformed by the method. The method is used for acquiring a plant cell transformed by an exotic gene. The present sequence represents Arabidopsis thaliana contains a plant cell present sequence represents Arabidopsis thaliana contains a plant cell present sequence represents Arabidopsis thaliana contains a plant cell present sequence represents Arabidopsis thaliana contains a plant cell present sequence represents Arabidopsis thaliana contains a plant cell present sequence represents Arabidopsis thaliana contains a plant cell present sequence represents a plant cell can be contained by the contained by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                           Matches
                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cis control sequence showing a capacity of controlling DNA damage-responding gene expression of a higher plant, a DNA damage-responding promotor, an expression cassette for a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-2001; 2001JP-00079524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2002272469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA damage-responding pr
transformed plant cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cis control sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS55373;
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a cis control sequence showing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 5; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NARA-) NARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-2001; 2001JP-00079524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                  damage-responding promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATAAAAAGCTTCTTCA
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      4
                                             15;
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                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAAAAAGCTTCTACA 26
                                                                                                                             44
    AAAAGCTTCTTCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana
                                                                                                                             BP; 10
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                             A; 11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAGAKU GIJUTSU DAIGAKUIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA damage-responding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%;
                                                              72.0%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA damage-responding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16
      19
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                                             0
                                                                 Score 14.4;
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yerresponding gene expression; plant expression cassette; ds.
                                                                                                                             <u>.</u>
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                                               Mismatches
                                                                                                                                13 T; 0 U; 0 Other;
                                                                     8.3e+03;
                                                                                        ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter sequence
                                                                                        6,
                                                                                      Length 44;
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                                                 Gaps
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ABS55383/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention relates to a cis control sequence showing a CC capacity for controlling DNA damage-responding gene expression of a CC higher plant, a plant (Arabidopsis thaliana) DNA damage-responding CC promoter, and an expression cassette for a plant. The invention describes CC an expression cassette for a plant for expressing an exotic gene, by CC responding to DNA damage containing the above promoter and a site for CC inserting an exotic gene, so that said exotic gene is linked to said CC promoter expressably. Also described is a recombinant plasmid for CC expressing an exotic gene by responding to DNA damage containing the CC expressing an exotic gene by responding to DNA damage containing the CC above promoter and an exotic gene linked expressably to said promoter, a CC method for acquiring a plant cell transformed by an exotic gene wherein a CC expression a plant cell with the above recombinant plasmid to get a CC transformed plant cell with the above recombinant plasmid to get a CC transformed plant cell, and a transformed plant cell prepared by the CC above method. The method is used for acquiring a plant cell transformed coll by an exotic gene. The present sequence represents a primer used in the CC examples of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
Cis control sequence showing a capacity of controlling DNA damage-responding gene expression of a higher plant, a DNA damage-responding
                                                                                                                                                                                                                JP2002272469-A.
                                                                                                                                                                                                                                                                                        Cis control sequence; DNA damage-responding gene expression; DNA damage-responding promoter; plant expression cassette;
                                                   WPI; 2002-718706/78
                                                                                                                19-MAR-2001;
                                                                                                                                                19-MAR-2001; 2001JP-00079524
                                                                                                                                                                                 24-SEP-2002
                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                               transformed
                                                                                                                                                                                                                                                                                                                                             Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                              16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABS55383 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                            ABS55383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cis control sequence showing a capacity of controlling DNA damage-responding gene expression of a higher plant, a DNA damage-responding promotor, an expression cassette for a plant.
                                                                                  (NARA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Page 12; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAGCTTCTTCAACA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAGGCTTCTTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP;
                                                                                                                                                                                                                                                                              plant
                                                                                                                                                                                                                                                                                                                                             thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                 SENTAN
                                                                                                                2001JP-00079524.
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENTAN KAGAKU GIJUTSU DAIGAKUIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                          cell; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 7 C; 5 G; 8 T; 0 U; 0 Other;
                                                                                 KAGAKU GIJUTSU
                                                                                                                                                                                                                                                                                                                                           DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                           primer -123/-118
                                                                                                                                                                                                                                                                                                                                                                                                                                         В₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.4; DB Pred. No. 8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                 DAIGAKUIN
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Altering deoxyribonucleic acid in a Sorangium host cell comprises transforming the host cell with a transposon vector comprising in

and

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gene encoding

a transposase

inverted

13-AUG-2002; 2002US-0403290P. 13-AUG-2003; 2003WO-US025364.

(KOSA-) KOSAN BIOSCIENCES INC

2004-169502/16

19-FEB-2004 WO2004015088-A2 Chrysoperla

carnea.

terminal repeat sequences (ITRs) recognizes the ITRs.

The invention relates to a

2

SEQ

ID NO

6;

28pp;

English.

Sorangium host cell. a transposon vector

cell.

encoding a transposase that recognizes

the ITRs,

where cell

the

host

. The method comprises transforming t containing inverted terminal repeat

method of altering deoxyribonucleic acid (DNA)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC capacity for controlling DNA damage-responding gene expression of a CC higher plant, a plant (Arabidopsis thaliana) DNA damage-responding CC promoter, and an expression cassette for a plant. The invention describes CC an expression cassette for a plant for expressing an exotic gene, by CC responding to DNA damage containing the above promoter and a site for CC inserting an exotic gene, so that said exotic gene is linked to said CC promoter expressably. Also described is a recombinant plasmid for CC expressing an exotic gene by responding to DNA damage containing the above promoter and an exotic gene linked expressably to said promoter, a CC method for acquiring a plant cell transformed by an exotic gene wherein a CC specific expression responding to DNA damage is desired including a step CC of transforming a plant cell with the above recombinant plasmid to get a CC transformed plant cell, and a transformed plant cell prepared by the CC above method. The method is used for acquiring a plant cell prepared by the examples of the present sequence represents a primer used in the crowd or containing a plant cell present sequence represents a primer used in the crowd or containing a plant cell present invention crowd or containing a plant cell present invention crowd or containing a plant cell transformed containing a plant cell present invention crowd crowd containing a plant cell transformed containing a plant ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transposon vector; pKOS183-3; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer 111-132.6, seq id 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ66058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a cis control sequence showing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ66058 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promotor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAGCTTCTTCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 BP; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGCTTCTTCAACA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an expression cassette for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 12; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal repeat sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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No. 86
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Canidae
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08-OCT-2004;
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                                                                                                                                                                                                                                                                                                                                                 infection; diabetes; hypertension; atherosclerosis; autoimmune disease;
renal disease; neurological disease; primer; ss.
                                                                                                                                                                                                                                                                                                                                                        animal breeding; genetic marker; SNP detection; allelic variation;
infection; diabetes; hypertension; atherosclerosis; autoimmune dis
                                                                                                                                                                                                                                                                                                                                                                       Canine SNP
                                                                                                                                                                                                                                                                  Rosenfeld D,
                                                                                                                                                                                                                                                                                                       25-OCT-2004; 2004WO-US035231
                                                                                                                                                                                                                                                                                                                             WO2005040350-A2
                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-2005
                                                                                                                                                                                                                                                                             (MMIG-) MMI GENOMICS
                                                                                                                                                                                                                                                                                                                                                                       detection, extension primer
                                                                                                                                                                                                                                                                                        2003US-0514180P.
2004US-0617383P.
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                  Kerr R,
                                                                                                                                                                                                                                                                  Hutton
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                                                                                                                                                                                                                                                                  Denise S,
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                                                                                                                                                                                                                                                                  Bates S,
                                                                                                                                                                                                                                                                                                                                                                        No:353
                                                                                                                                                                                                                                                                   Fantin
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markers Identifying animal genetic marker that influences trait for determining parentage or to infer breed/line in e.g. canines involves analyzing markers of genome-wide genetic marker map for association with genetic

WPI; 2005-333502/34

Claim 45; SEQ ID NO 353; 145pp; English

CC series of oligonucleotides that bind at or near a genomic location of the series of companion animal SNPs, a mechanism for moving the solid support or other hybridization medium, and a liquid handling CC mechanism for applying a liquid to the series of oligonucleotides, CC diffected by the nucleotide to a polynucleotide to a liquid handling CC determining nucleotide occurrences of the SNP; (ii) a kit for CC determining nucleotide occurrences of canine SNPs, comprising an CC oligonucleotide occurrence of at least one canine SNPs, comprising an CC distances given as SEQ ID Nos 1-101 in the specification; (iii) a determining to the most 3' position of nucleotide or complement in the most 3' position of nucleotide or complement in the specification; (iii) a computer-based method for identifying/inferring a trait of CC complement in the nucleotide occurrence of at least one successive of a canine state one nucleotide occurrence of at least one successive of corresponding to the first nucleotide, or complement is to first nucleotide, or complement is to first nucleotide occurrence of at least one SNP corresponding trait of CC acain to the first nucleotide, or complement its in the most 3' position of nucleotide sequences in SEQ ID Nos 1-101, searching a CC optionally storing to the first nucleotide, or complement its in the most 3' consistion of nucleotide sequences in SEQ ID Nos 1-101, searching a computation may be subsequently accessed and viewed by the user, and identifying the trait of a canine subject; (v) an isolated with a CC sadditional nucleotide sequences in SEQ ID Nos 1-101; to complement its complement CC with nucleotide sequences in SEQ ID Nos 1-101; or a first nucleotide or its complement CC derived from a canine subject, or a first nucleotide or its complement CC orresponding to the first nucleotide or complement in the most 3' position of any one of the nucleotide or its complement CC orresponding to the first nucleotide or complement in the most 3' position of a nucleotide or the first nucleotide companion animal genetic markers of a genome-wide genetic marker map for association with the genetic trait and identifying the companion animal genetic marker that influences the trait. Also described are: (i) a high throughput system for determining the nucleotide occurrences at a series The invention relates to a method of identifying of companion animal SNPs comprising a hybridization medium containing a marker relates to a method of identifying a companion animal that influences a phenotype or trait comprising analyzing

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cc identifying in the nucleic acid sample at least one SNP corresponding to cidentifying in the nucleic acid sample at least one SNP corresponding to corresponding to each SNP identified, and comparing the alleles to corresponding to each SNP identified, and comparing the alleles to corresponding to each SNP identified, and comparing the alleles to comparing the least one allele in common with the test subject are excluded, and (x) the use of a first primer selected from SEQ ID Nos 102-203, and a second primer selected from SEQ ID Nos 102-203, and a comparing the method of the cinvention. The method is useful for identifying a companion animal comparing to an invention. The method is useful for identifying a companion animal comparing to an invention, susceptibility to infection, regulation of immune status and cresponse to antigens, previous exposure to infection or parasites, companion animal (preferably dogs, cats, fish, reptiles, birds, horses, cantoimmune disorders, kidney disease and neurological disease in companion animal (preferably dogs, cats, fish, reptiles, birds, horses, candidate, maximizing individual potential performance and health, allowing predictive (predisposition) diagnostics, mutritional therapies and collective (predisposition) diagnostics, mutritional naimal owners and collective profits related to selling a companion animal owners and collective such as energy metabolism, aging and breed-specific traits to track a companion animal profits, to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits to track a companion animal or of specific traits or the
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genetic trait, to track a companion animal or offspring, and to dia
a health condition of a companion animal. This sequence represents
extension primer used for the detection of canine SNPs.
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Sequence 25 BP; 5 A; 2 C; 5 G; 13 T; 0 U; 0 Other;

Query Match Best Local S Matches 15 15; Similarity Conservative 72.0**%**; 93.8**%**; 0 Score 14.4; DB 14; Pred. No. 7.9e+03; Mismatches Length 25; 0; Gaps 0

20 4 AAAAGCTTCTACAACA AAAAGCTTCTTCAACA 19

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KESULT 25 ABS55388 ABS55388 standard; DNA; 29 Arabidopsis thaliana DNA, primer -94/-89 16-DEC-2002 (first entry)

Cis control sequence; DNA damage-responding transformed plant sequence; DNA damage-responding gene expression; cell; promoter; plant expression cassette;

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Arabidopsis thaliana

24-SEP-2002

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RESULT 22
AAL51795
ID AAL51
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Matches 16
Query Match
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                                                                                                                                   The invention comprises the amino acid and coding sequence of the histone acetyl transferase 21.67 protein. The DNA and protein sequences of the invention are useful for the treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The
                                                            Sequence
                                                                                                                                                                                                                                      Example
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invention are useful for the treat
HIV infection, immunological disea
present DNA sequence represents a
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                                                            B₽;
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                                                                                                                                                                                                                                                                           polypeptide.
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74.0%;
88.9%;
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88.9%;
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Pred. No. 5.4e
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Pred.
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                                                          10 T; 0 U; 0 Other;
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14.8; DB 6;
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ADZ97756/c ID ADZ977 XX

ADZ97756

standard;

DNA;

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ВP

RESULT

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RESULT 23
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                                                                                                                                The present sequence is that of PCR primer INGEN 8_3, corresponding to nucleotides 2544-2565 of the hamster islet neogenesis gene associated protein (INGAP) gene. It is one of a set of primers (see ACF05852-71) used to generate PCR fragments of the INGAP gene, which were subsequently sequenced to determine the nucleotide sequence (see ACF05851) of the INGAP 5' regulatory region, the introns, the intron/exon junctions, and the 3' polyadenylation region. The 5' regulatory region of the INGAP gene is susceptible to modulation by many known transcription factors, and is used in claimed screening assays to identify agents capable of modulating INGAP gene expression. These modulating agents have potential as therapeutic agents for treating type 1 and type 2 diabetes mellitus, endocrine and non-endocrine hypoplasia, hypertrophy, adenoma, neoplasia
                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                         New isolated INGAP nucleic acid, useful for diagnosing and treating disorders associated with reduced islet cell function and/or aberrant expression or activity of INGAP, such as type II diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2002; 2002US-0346898P
01-MAR-2002; 2002US-0361073P
14-JUN-2002; 2002US-0388315P
                                                                                                                                                                                                                                                                                                      Example 1;
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-598524/56.
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses a microarray comprising a plurality of nucleic cc acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used compounds: The nucleic acid probes are specifically designed for analysis of genetic variation or in hybridisation to a DNA library, compounds: The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises compounds: The content of the method of analysis comprises of a probes and detecting the hybridisation. The nucleic acid probes and the hybridisation. The nucleic acid grobes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, comparisor acid gene expression levels, identifying biallelic markers or polymorphisms, comparisor acid gene expression to identify or detect the sequence. Each of the nucleic acid solid surport at stag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotlothybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been concleic acid probes incorporated in the microarray. Note: The sequence or specific acid at for this patent can also be obtained in electronic format directly at a gardara unarto, acceptance at the sequence of the sequence at a gardara unarto, acceptance at the sequence of the sequence at a gardara unarto, acceptance at the sequence of the sequence at a gardara unarto, acceptance at the sequence of the sequence at a gardara unarto, acceptance at the sequence of the sequence at a gardara unarto, acceptance at the sequence of the sequence at a gardara unarto, acceptance at the
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      AAL51793 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                  11 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
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Pred. No. 5.2e+03
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                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequence of the histone acetyl transferase 21.67 protein. The DNA and protein sequences of the invention are useful for the treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various inflammations. The process of the acetyl transferase are the acetyl transferase are the acetyl transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer; PCR; histone acetyl transferase; enzyme; 21.67; malignant tumour; haemopathy; HIV; immunological disease; inflammation; ss.
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                                                                                 CN1361260-A.
                                                                                                                          Probe; ss; histone acetyl transferase; enzyme; 21.67; malignant tumour; haemopathy; HIV; immunological disease; inflammation.
                                                                                                                                                        Histone acetyl transferase 21-67 nucleotide probe
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                                                                                                                                                                                                                                                                                                                                                            Sequence 33
                                                                                                                                                                                                                                                                                                                                                                                 present DNA
21.67 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 18 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histone acetyl transferase encoding this polypeptide.
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                    26-DEC-2000;
                                         26-DEC-2000;
                                                              31-JUL-2002
                                                                                                       Unidentified
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(BODE-) BODE GENE DEV CO LTD SHANGHAI
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Matches 17
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Best Local :
                                                                                                                                                                                         The invention relates to a DNA (I) that shows increased or decreased expression during biosynthesis of cell wall components or formation of wood fibre cells in a plant, comprising a nucleotide sequence that hybridises under stringent conditions with any of 1731 fully defined sequences (S1) of 60 nucleotides given in specification, or with a nucleotide sequence encoding a protein having 50% or more homology with that encoded by (S1). Also included in the specification are: (a) a promoter DNA (II) of (I); (b) a DNA comprising a nucleotide sequence that is complementary to (I) or nucleotide sequence that codes RNA, which suppresses the expression of (II by RNA interference effect or the cosuppression effect; (c) a recombinant vector (III) comprising (II); (d) a microorganism comprising (III); (e) a transformed print cell (IV) comprising (III); are areas and (f) a transformed print of (V) obtained from (IV).
                                                                                                                                                   (I) are useful for regulating biosynthesis of cell wall components or morphological formation of wood fibre cells. This sequence corresponds an expressed sequence tag (EST) fragment relating to the DNA of the
                                                                                                            Sequence 60
                                                                                                                                                                                                                                                                                                                                                                                                                      New genes specifically expressed in eucalyptus wood forming tissues, useful in controlling biosynthesis of cell wall components and morphological formation of wood fiber cells.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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57
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wood fibre cell; plant; eucalyptus.
                                                                                                             BP;
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85.0%;
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Pred. No. 3
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Pred. No. 3.5e+03;
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                                                                               DB 13; Length
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                                                      Indels
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                                                                                                                                                      ce corresponds to DNA of the
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                                                    Gaps
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RESULT 18
ACK18857
ID ACK18
XX ACK18
AC ACK18
XX EST;
XW EST;
XW Genet
XX Cross
OS Homo
XX US200
XX US200
XX 16-M2
PD 05-JU
XX 16-M2
XX 16-M2
XX I6-M2
XX RPF;
XX WPI;
XX New a
PT South
PT seque
XX Clain
                                                                                                                                                                                                                                                                                                                                      The invention discloses a microarray comprising a plurality of nucleic caid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, city in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridisation probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, cor family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dotblot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence of the sequence of the sequence and slob be obtained in electronic format directly
                                                                                                                              Best Loc
Matches
                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                         Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 118838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-567953/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2002; 2002US-00098263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                  USPTO at seqdata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray
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                                                                                                                              16;
                                                                                                                                                               Similarity
                                                               AAAAAGCTTCTTCAACAC
                                                                                                                                                                                                                                                         BP; 11 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                     74.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽P
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Pred. No. 5.
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                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in situ hybridization, to identify or detect
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Claim

c C

39; 31pp;

English

Sequences AAA06974-A07013 represent antisense oligonucleotides targetted CC to the human Smad5 gene, which inhibit its expression. The antisense CC oligonucleotides were designed to target different regions of the human CC Smad5 RNA, and were analysed for their effect on Smad5 mRNA levels by CC quantitative real-time PCR. The Smad proteins are a family of cytosolic proteins which are involved in TGF-beta superfamily signal transduction. CC On ligand binding, TGF-beta superfamily proteins (such as bone morphogenetic protein (BNP), activin and TGF-betas themselves) CC phosphorylate Smad proteins, which then homo- or heterodimerise and CC translocate to the nucleus to activate target gene transcription. Smad5 CC (also known as MADH5, Dwarfin-C and JV5-1) is a member of the subgroup of CC Smad family transcription factors which mediate signal transduction from CC SMPs. Smad5 is activated by BNP-2 through the BNP type Ia or Ib CC (US6013787; AN769622) and translocate to the nucleus. The antisense CC oligonucleotides of the invention are useful for diagnosis, prevention CC and treatment of conditions associated with Smad5 expression, such as CC tumour formation, inflammation and certain infections

of.

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ADAMS9127
ID ADAMS9127
ID ADAMS9127
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AC ADAMS
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19-AUG-1999;
09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; infection; diagnosis; th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria ORF4 lipoprotein PCR primer orf4-L for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA89127 standard; DNA; 33
This oligonucleotide, termed orf4-L for, is used as forward primer, withe reverse primer given in AAA89128, for the PCR amplification of ORF lipoprotein of a Neisseria sp. The PCR product was used in expression purification experiments, and can be used as 1 component of novel
                                                                                                                                                                                                                                                                                                                                                                                                                                              Giuliani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-2000; 2000WO-IB000828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200071725-A2
                                                                                                                                                                     Example
                                                                                                                                                                                                                                 Neisseria bacterium, useful as treating Neisserial infections.
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-025167/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-)
                                                                                                                                                                                                                                                                        composition comprising first and second biological molecules from eria bacterium, useful as vaccines or immunogenic compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIRON
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                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000GB-00005730
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Pizza
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99GB-00019705.
                                                                                                                                                                     60; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Rappuoli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ria gonorrhoeae; ORF4; lipoprotein; vaccine; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                          R
                                                                      forward primer, wit mplification of ORF4
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The invention relates to methods for the heterologous expression of Neisserial proteins from Neisseria meningitidis and Neisseria gonorrhoeae. At least one domain in the protein is deleted, e.g. the leader peptide, and may be replaced by a domain from a different protein to make a fusion protein, in order to enhance heterologous expression of Neisserial proteins. Also, a region of a protein, such as a poly-glycine stretch, can be mutated to enhance expression. The proteins used in the processes include ORF46.1, 287, 741, 919, 953, 961 and 983. Sequences AAS43807-AAS43867 and AAS43906-AAS44358 represent PCR primers used in the

Disclosure;

Page 81; 119pp;

English

Sequence 33

BP; 11

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methods of the

invention A; 11

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AAS43911
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                combination compositions of the invention. These compositions comprise: (i) 2 or more Neisserial proteins, (ii) 2 or more different Neisserial nucleic acids; or (iii) mixtures of 1 or more Neisserial protein and 1 or more Neisserial nucleic acid. The proteins and nucleic acids are preferably from different Neisseria spp., especially Neisseria meningitidis and Neisseria gonorrhoeae, but may be from the same species, or from different serogroups or strains of the same species. The compositions are used e.g. as immunogenic compositions, vaccines or diagnostic reagents. They are used to treat or prevent Neisserial infection, to detect the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria, and/or as reagents which can raise
                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria g
Neisserial
                                                                                                                                                                                                                     Arico
Pizza
                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis B MC58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies against Neisserial bacteria
                                                                                                                                                                                               WPI; 2001-582163/65
                                                                                                                                                                                                                                                                          28-FEB-2000;
13-NOV-2000;
                                                                                                                                                                                                                                                                                                          28-FEB-2001; 2001WO-IB000452
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                                                                                                                                                                                                                                                                                                                                                      WO200164922-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
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                                                                                                                                                                           Producing
                                                                                                                                                                                                                                                      (CHIR-)
                                                                                                                                                                                                                     , WB
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                                                                                                                                                                                                                                                      CHIRON SPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAAAAAGCTTCTTCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                  gonorrhoeae; leader peptide;
                                                                                                                                                                         heterologous
                                                                                                                                                                                                                               Comanducci
                                                                                                                                                                                                                                                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 11 A; 11 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                         2000GB-00004695.
2000GB-00027675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer
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85.0%;
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                                                                                                                                                                           proteins from Neisseria meningitidis
                                                                                                                                                                                                                                 Galeotti
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence PCR
                                                                                                                                                                                                                                                                                                                                                                                                                       fusion
                                                                                                                                                                                                                                 Masignani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ა</u>
                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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                                                                                                                                                                                                                                  Guiliani
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4 AAAAGCTTCTTCAACAC 20

Query Match Best Local Matches

Similarity

77.0%; 94.1%; 6 C; 2

Score 15.4; Di Pred. No. 2.7e. 0; Mismatches

2.7e+03; DB 3;

Length Indels

0

Gaps

0;

Conservative

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Sequence

18 BP; 7

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G; 3 T; 0

U; 0 Other;

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RESULT 13
ADK67815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transferring, to a mutant strain of microorganism from which any of Bacillus subbilis genes have been deleted or knocked out, a gene encoding a heterologous protein or polypeptide. The recombinant microorganism and method are useful for producing a protein or polypeptide of interest or substances, e.g. food, antibiotics, sugars, or lipids. The present sequence represents a Bacillus PCR primer.
                       01-AUG-2002; 2002US-0400892P
29-JUL-2003; 2003US-00630154
                                                                                       31-JUL-2003; 2003WO-US024218
                                                                                                                                      12-FEB
                                                                                                                                                                               WO2004013357-A2
                                                                                                                                                                                                                           Francisella tularensis
                                                                                                                                                                                                                                                                  Tularaemia; biological
                                                                                                                                                                                                                                                                                                                 Francisella
                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADK67815 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant microorganism prepared by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant microorganism of genus E protein of interest or substances, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2003; 2003JP-00379167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus PCR primer SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tohata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2005045013-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KAOS )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ξ¥
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAAAAAGCTTCTTCAAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ďs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sawada K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                              tularensis hybridisation probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004WO-JP016891
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ╏
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotic; sugar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 A; 12 C; 3 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozaki
                                                                                                                                                                                                                                                                     weapon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.4; DB Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                     detection; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kobayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus, useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to detect the specific F. tularensis nuclectide sequence, especially using a fluorogenic 5' nuclease PCR assay. The invention provides different primer/probe sets for different loci on the F. tularensis genome. Also provided is a method for identifying F. tularensis by analysing samples taken from monitoring devices, such as air monitors for nucleotide sequences that are specific to the bacterium. As the nucleotide sequences are unique to F. tularensis, the primers/probes provide a more reliable method of detection than existing methods, reducing the occurrence of false positive and false negative results.
            Novel antisense compounds useful for inhibiting the in human cells or tissues and treating inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of a hybridisation probe for a specific Francisella tularensis nucleotide sequence ADK67816 that serves as a marker or signature for identification of the bacterium. F. tularensis the causative agent of tularaemia and a potential weapon of mass destruction and instrument of terror. A PCR forward primer ADK67813, reverse primer ADK67814 and the present hybridisation probe can be used
                                                        WPI; 2000-270139/23.
                                                                                                                                         23-FEB-1999;
                                                                                                                                                                   23-FEB-1999;
                                                                                                                                                                                              21-MAR-2000.
                                                                                                                                                                                                                         US6040178-A
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                            transcription
                                                                                                                                                                                                                                                                                                          Smad5; MADH5;
                                                                                                                                                                                                                                                                                                                                    Human Smad5 phosphorothioate antisense oligonucleotide,
                                                                                                                                                                                                                                                                                                                                                                 03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                            AAA07003
                                                                                                                                                                                                                                                                                                                                                                                                                        AAA07003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising an Amplicon that is a single strand sequence of nucleic acids specific to Francisella tularensis, useful for detecting Francisella tularensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mccready PM, :
Kuczmarski TA,
                                                                                                               (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                               inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; SEQ ID NO 31; 29pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
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                                                                                   ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAAAAGCTTCTTCAACA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAAGAGCTTCTTCAACA 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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, Vitalis E
                                                                                                                                                                                                                                                                               antisense; ss
                                                                                                                                                                                                                                                                                          Dwarfin-C; JV5-1; TGF-beta sign factor; expression inhibition;
                                                                                                                                         9905-00256492
                                                                                                                                                                    99US-00256492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 8 C; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                            TGF-beta signalling n inhibition; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ġ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Slezak
            expression and tumor f
                                                                                                                                                                                                                                                                                             pathway;
formation;
                                                                                                                                                                                                                                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monitors,
                                                                                                                                                                                                                                                                                                                                      NO:37
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formation of Smad5

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RESULT 10
AEA02869
ID AEA02
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            transferring, to a mutant strain of microorganism from which any of Bacillus subtills genes have been deleted for knocked out, a gene enco a heterologous protein or polypeptide. The recombinant microorganism method are useful for producing a protein or polypeptide of interest substances, e.g. food, antibiotics, sugars, or lipids. The present
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-347061/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2004; 2004WO-JP016891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-2005
                                                                                                                                  07-NOV-2003;
                                                                                                                                                   05-NOV-2004; 2004WO-JP016891
                                                                                                                                                                                                         Bacillus
                                                                                                                                                                                                                                            Bacillus PCR primer SEQ ID
                                                                                                                                                                                                                                                               28-JUL-2005
                                                                                                                                                                                                                                                                                 AEA02869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of interest or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant
                                                   protein
                                                    New recombinant microorganism of genus Bacillus, protein of interest or substances, e.g. food, ant
                                                                                               Tohata M,
                                                                                                                                                                      19-MAY-2005
                                                                                                                                                                                      WO2005045013-A2
                                                                                                                                                                                                                                                                                                   AEA02869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAOS
                                                                                                                 (KAOS ) KAO CORP.
                                                                                                                                                                                                                          PCR;
                                                                               2005-347061/35
                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Σ,
                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
17; Conserv
                                                                                                                                                                                                                           food;
                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                        ATAAAAAGCTTCTTCAAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                   45 BP; 14 A; 10 C; 5 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     represents a Bacillus PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 118; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sawada K,
                                                                                                Sawada K,
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003JP-00379167
                                                                                                                                  2003JP-00379167
                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to a recombinant microorganism
                                                                                                                                                                                                                           antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microorganism of gorest or substances,
                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                        82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ozaki
                                                                                                 Ozaki
                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                           sugar;
                                                                                                                                                                                                                                             NO 112
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                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genus E
                                                                                               Kobayashi
                                                                                                                                                                                                                           primer.
                                                                                                                                                                                                                                                                                                                                                                                         16.4; DB:
No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus, food, ant
                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
                                                                                                ζ,
                                                                                                                                                                                                                                                                                                                                                                                  ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us, useful for antibiotics, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogasawara
                                                    us, useful for
antibiotics,
                                                                                                Ogasawara
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepared
                                                    for producing
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                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r producing sugars, or
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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The invention Example 1;

relates to a recombinant microorganism prepared by to a mutant strain of microorganism from which any

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AEA02855 RESULT 12

AEA02855 standard;

DNA;

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SEQ

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112;

62pp; English.

transferring,

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RESULT 11
AEA02849
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                                     Query Match
Best Local S
Matches 17
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis genes have been deleted or knocked out, a gene encoding a heterologous protein or polypeptide. The recombinant microorganism and method are useful for producing a protein or polypeptide of interest or substances, e.g. food, antibiotics, sugars, or lipids. The present
                                                                                                                                                                                                  New recombinant microorganism of guprotein of interest or substances, lipids.
                                                                                                                                                                                                                                                                                                                                                                  WO2005045013-A2
                                                                                                                                                                                                                                                                                                                                                                                      Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                         88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a Bacillus PCR primer.
                                                                                                         a heterologous protein or polypeptide. The recombinant microorganism method are useful for producing a protein or polypeptide of interest substances, e.g. food, antibiotics, sugars, or lipids. The present
                                                                                                                                      The invention relates to a recombinant microorganism prepitransferring, to a mutant strain of microorganism from who Bacillus subtilis genes have been deleted or knocked out.
                                                                                                                                                                                                                                            WPI; 2005-347061/35
                                                                                                                                                                                                                                                                Tohata
                                                                                                                                                                                                                                                                                                        07-NOV-2003;
                                                                                                                                                                                                                                                                                                                          05-NOV-2004; 2004WO-JP016891
                                                                                                                                                                                                                                                                                                                                               19-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA02849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEA02849
                                                                             Sequence
                                                                                                                                                                                Example 1;
                                                                                                                                                                                                                                                                                    (KAOS ) KAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 ATAAAAACCTTCTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
 16
                                                                                                                                                                                                                                                                Z,
                                      l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAAAAAGCTTCTTCAAC
                                                                              45
                                                                                                                                                                                                                                                                                                                                                                                                         food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 45
               ATAAAAAGCTTCTTCAAC
                                                                                                 represents a Bacillus PCR primer.
                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                Sawada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                              B₽;
                                                                                                                                                                                                                                                                                    CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                        2003JP-00379167
                                                                                                                                                                                                                                                                                                                                                                                                                          primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                ID NO 92; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 A; 11 C; 4 G;
                                                                              19
                                                                                                                                                                                                                                                               ζ,
                                                                              A; 11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
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94.4%;
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s, e.g.
                                                                                                                                                                                                                                                               Kobayashi
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                                                 16.4;
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1e+03;
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  Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to antisense compounds, compositions and methods for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition comprises antisense compounds that can be targeted towards HDAC2. The compound is useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer. It is also useful in antisense gene therapy. The present sequence is human HDAC2 DNA target region. Human HDAC2 gene is located at chromosome 6q21.
                                                                                     antisense;
                                                                                                                                          Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3;
                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                            15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New compound, having a sequence targeted to a coding region of a nucleic acid encoding human histone deacetylase 2, useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer.
                                                                                                                  hyperproliferative
                                                                                                                                                                                                                                                                                                                 ADN49072;
                                                                                                                                                                                                                                                                                                                                                                         ADN49072 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MONI/) MONIA B P. (DOBI/) DOBIE K W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUN-2002; 2002US-00173192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human histone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAGCTTCTTCAACAC
                                                                                     phosphorothioate backbone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dobie KW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 5 A; 1 C; 6 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                 specific antisense oligo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                         (first
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                                                                                                                  disorder;
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                                                                                                               cancer; antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; antisense gene therapy; human;
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                                                                                                         therapy; human;
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               WO2005045013-A2
                                              Bacillus
                                                                                                         Bacillus
                                                                                                                                       28-JUL-2005
                                                                                                                                                                     AEA02875;
                                                                                                                                                                                                  AEA02875
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compound, having a sequence targeted to a coding region of acid encoding human histone deacetylase 2, useful for preparing composition for treating hyperproliferative disorders, e.g., car
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modified_base
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17; Conserv
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DOBIE K W.
                                                                                                                                                                                                  standard; DNA;
                                                                                                                                                                                                                                                                                                  AAAAGCTTCTTCAACAC
                                                                          food;
                                                                                                       PCR primer SEQ ID NO 118
                                                                                                                                                                                                                                                                               AAAAGCTTCTTCAACAC
                                                                                                                                                                                                                                                                                                                                                                                                      BP; 8 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 43;
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                       (first
                                                                         antibiotic; sugar; primer.
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/mod_base= OTHER
/note= "2'-methoxyethyl bases"
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/note= "Phosphorothioate backbone in which all cytidines
are 5-methylcytidines"
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/mod_ba
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e= "2'-methoxyethyl bases"
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. 5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperproliferative disorder; cancer; apoptosis; metabolic disorder; antisense-therapy; cytostatic; antiinflammatory; human; phosphorothioate backbone; antisense; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human histone deacetylase 2 DNA antisense oligo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_base
                                                                                                                                                                                                                                New antisense oligonucleotide compound, useful for diagnosing, preve and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2002; 2002US-00173192
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The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder
                                                                                                                                                                                                                                                                                                                                                                                Monia BP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-2002;
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                                                                                                                                                                                         Example 15; SEQ ID NO 43; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-00173192
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16. .20
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                                                                                   The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder The invention is also useful in antisense-therapy. The present sequence is human histone deacetylase 2 target DNA fragment used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotide compound, useful for diagnosing, p and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disord
                                                                                                                                                                                                                                                                                                                                                                                            Example 15; SEQ ID NO 67; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-070606/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human histone deacetylase 2 target DNA fragment
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                                                             exemplification
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24-NOV-2003;
24-NOV-2003;
03-DEC-2003;
14-JAN-2004;
10-FEB-2004;
                         interference. Also disclosed are an expression vector comprising a nucleic acid sequence encoding an siNA molecule; and a mammalian cell comprising the expression vector. The siNA molecule (I) is useful for modulating the expression. It is also useful for modulating the expression and activity of other genes in the pathways of RAS. The siNA molecule is also useful for diagnosing or treating diseases and conditions that respond to the modulation of RAS gene expression or
                                                                                                                                                                                                                                                                           The invention describes a chemically synthesized double stranded short interfering nucleic acid (siNA) molecule (I) that directs cleavage of a RNA via RNA interference (RNAi), where each strand of the siNA molecule is 18-23 nucleotides in length, and one strand of the siNA molecule comprises nucleotide sequence complementary to the N-RAS RNA the siNA molecule to direct cleavage of the N-RAS RNA via RNA in the sinA molecule to direct cleavage of the N-RAS RNA via RNA
       activity, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New chemically synthesized double stranded short interfering nucleic acid molecule that directs cleavage of N-RAS RNA via RNA interference, useful for modulating RAS gene expression.
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30-APR-2004;
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; 2003US-00720448.
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           cancer or other
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expression or disorders, or
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Best Local
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24-MOV-2003; 2003US-00720448.
03-DEC-2003; 2003US-00727780.
14-JAN-2004; 2004US-00757803.
10-FEB-2004; 2004US-0543480P.
13-FEB-2004; 2004US-00780447.
16-APR-2004; 2004US-00826966.
30-APR-2004; 2004WO-US013456.
24-MAY-2004; 2004WO-US013490.
interference. Also disclosed are an expression vector comprising a nucleic acid sequence encoding an sinA molecule; and a mammalian cell comprising the expression vector. The sinA molecule (I) is useful for modulating RAS gene expression. It is also useful for modulating the expression and activity of other genes in the pathways of RAS. The sinA molecule is also useful for diagnosing or treating diseases and conditions that respond to the modulation of RAS gene expression or activity, e.g. cancer or other proliferative diseases, disorders, or conditions. This sequence represents a human N-Ras siRNA target sequence
                                                                                                                       The invention describes a chemically synthesized double stranded short interfering nucleic acid ($iNA) molecule (I) that directs cleavage of an example of the sina molecule is 18-23 nucleotides in length, and one strand of the sina molecule comprises nucleotide sequence complementary to the N-RAS RNA the sina molecule to direct cleavage of the N-RAS RNA via RNA the sina molecule to direct cleavage of the N-RAS RNA via RNA
                                                                                                                                                                                                                                              New chemically synthesized double stranded molecule that directs cleavage of N-RAS RNZ for modulating RAS gene expression.
                                                                                                                                                                                                                     Claim 33; SEQ ID NO 363; 204pp; English.
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RESULT 1
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The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder
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Synthetic.
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                                                                                                                               New antisense oligonucleotide compound, useful for diagnosing, and/or treating conditions with aberrant activity of the histor deacetylase 2, such as cancer, inflammation and metabolic disco
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                                                                                                                          treating conditions with place 2, such as cancer.
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disorder

compound is useful

for preparing

The invention Example 15; composition

relates to antisense

compounds,

compositions

HDAC2

18

SEQ ID for treating

ö

32;

47pp;

English.

for modulating the expression of histone deacetylase 2 (HDAC2). HDI also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition comprises antisense compounds that can be targeted towards HDAC2.

can be targeted composition for

treating

New compound, acid encoding

having a sequence targeted to a coding region of a nucleic human histone deacetylase 2, useful for preparing a

hyperproliferative

disorders,

for preparing lers, e.g., car

cancer.

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RESULT 2
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Adj66058 Primer 11
Aad52829 Human Mow
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Aal28073 Human SNP
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1 (bases 1 to 27)

Le,J., Vilcek,J., Dad

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Le,J., Vilcek,J., Dadonna,P., Ghrayeb,J., Knight,
Methods of treating TNF-.alpha.-mediated Crohn's
chimeric anti-TNF antibodies
Patent: US 5656272-A 10 12-AUG-1997;
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nilarity 80.0%;
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/mol_type="unassigned DNA"
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                                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned
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                                from patent US
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                                                                                                                                  ; Score 13.6; D
; Pred. No. 3.6e
0; Mismatches
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Pred. No. 3.6e+05;
0; Mismatches 4;
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Matches 16; Conservat
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Adams,C.W., Carter,P.J., Fendly,B.M.
Agonist antibodies
Patent: US 6342220-A 17 29-JAN-2002;
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Sequence 10 from patent US 6790444.
AR580714
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Adams,C.W., Carter,P.J., Fendly,B.M. and Gurney,A.L.
Agonist antibodies
Patent: US 6737249-A 17 18-MAY-2004;
Genentech, Inc.; South San Francisco, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 from patent US AR540638
                           le,J., Vilcek,J., Daddona,P., Ghrayeb,J.,
Le,J., Vilcek,J., Daddona,P., Ghrayeb,J.,
Anti-TWF antibodies and peptides of human
Patent: US 6790444-A 10 14-SEP-2004;
New York University Medical Center and Cen
Location/Qualifiers
1. . . 27
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Location/Qualifiers
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/mol_type="genomic
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/organism="unknown"
/mol_type="genomic |
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pred. No. 3.6e+05;
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Pred. No. 3.6e+05;
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                                                     Inc.; New York,
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Sequence 3197 from I
AX485897
AX485897.1 GI:22320
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AX494015
Sequence
AX494015
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Candida albicans
Eukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                             Roemer,T., Jiang,B., Boone,C., Bussey,H. and Ohlsen,K.L. Gene disruption methodologies for drug target discovery Patent: WO 02053728-A 3197 11-JUL-2002; Elitra Pharmaceuticals, Inc. (US)
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Oligonucleotide library for detecting
variants that populate a transcriptome
Patent: WO 0210449-A 7476 07-FEB-2002;
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Mammalia; Eutheria;
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                                                                                                             TAAAAAGCTTCTTCAAC 18
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                                                                                                                                       Conservative
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              989
                                                                                                                                                                                                 /organism="Candida albicans"
/mol_type="unassigned DNA"
/db_xref="taxon:5476"
                                                                                                                                                                                                                                                  Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 2.5e+05;
0; Mismatches 2;
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Pred. No. 2.6e+05;
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WO02059355
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WO0210449.
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WO02053728.
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ORIGIN

Query Match Best Local S Matches 16

l Similarity
16; Conserv

Conservative

68.0%;

Score 13.6; DB 6; Pred. No. 3.6e+05; 0; Mismatches 4

6

Length 27;

Indels

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Patent: JP 2001513999-A 9 1:
GENENTECH INC
OS Homo sapiens (human)
PN JP 2001513999-A/9
PN JP 2001513999-A/9
PP 21-SEP-2001
PF 21-AUG-1998 JP 2000507/
PR 25-AUG-1997 US 08/9:
PI CAMELLIA W ADAMS, PAUL OF CC C12N15/09, A61K31/711, AMADAMS, PAUL OF C12N15/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agonist antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 27)

Adams, C.W., Carter, P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct synthetic construct
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Key
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JP 2001513999-A/9

11-SEP-2001

21-AUG-1998 JP 2000507802

25-AUG-1997 US 08/918148

CAMELLIA W ADAMS, PAUL J CARTER, BRIAN M FENDLY, AUSTIN L GURNEY

CL2N15/09, A61K31/711, A61K39/395, A61P7/00, A61P7/04, A61P7/06, PC
                                                                                                                                                                                                                                                                                                                               C07K16/28, C07K17/00, C07K19/00, C12N5/10, C12P21/08, C12N15/00,
                                                                                                                                                                        source
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                                                                                                                                                                                                                                                 therapeutic use
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                          /organism='Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Pred. No. 3.7e+05;
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and therapeutic
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Pull-length cDNAs
Patent: EP 1293569-A 3375 19-MAR-2003;
Helix Research Institute (JP); Resear
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Burczynski,M., Twine,N., Dorner,A.J. and Trepicchio,W.L. METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i Patent: WO 2004072265-A 1758 26-AUG-2004; Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. Dorner, Andrew J. (US); Trepicchio, William L. (US)
                                                                                                                                                                    CQ863125
Sequence 1758 from Patent
CQ863125
CQ863125.1 GI:51984114
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                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                          Homo sapiens (human)
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/db_xref="taxon:32630"
/note="an artificially synthesized
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/mol_type="unassigned_DNA"
/db_xref="taxon:32630"
/noTe="Artificially Synthesized
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88.2%;
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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                    Score 13.8; DB |
Pred. No. 3e+05;
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                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                            Submitted (21 NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE FOR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ523045.1 GI:26791281
left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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12446565
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                                    TANAAAGCTTCTTCAAC 18
   TAAAAACCTTCTTCCAC
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                                                                          Conservative
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/mol_type="unassigned DN/
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                                                                                                                                                               /note="T-DNA
left border"
                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
                                                                                                                                                                                                                     /ecotype="Wassilewskija"
                                                                                                                                                                                                                                          /clone_lib="Arabidopsis thaliana T-DNA
                                                                                                                                                                                                                                                         clone="305B04"
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                                                                        Score 13.8; DB 15;
Pred. No. 2.6e+05;
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AX081663
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        AR583303
Sequence 1230 from patent
AR583303
AR583303.1 GI:56619644
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synthetic construct
other sequences; artificial sequences.
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                                                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="unassigned DNA"
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Pred. No. 1.8e+05;
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Pred. No. 1.9e+05;
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involved in arachidonic acid metabolism
Patent: US 6794143-A 1230 21-SEP-2004;
Genset S.A.;;
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Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishi
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. an
                                                   synthetic construct
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other sequences; artificial sequences.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 1.7e+05;
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                                          Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide
methods of use thereof
Patent: WO 0147944-A 1281 05-JUL-2001;
Curagen Corporation (US)
                                                                                                                                                                          Sequence 1281 from Patent CQ002641 GI:41009273
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                                                                                                                                                                                                                                                                                                                                                                                               Multispecific and multivalent antigen-binding Patent: US 6476198-A 25 05-NOV-2002; The Scripps Research Institute; La Jolla, CA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Kang, A.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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/mol_type="genomic"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                 /organism="unknown"
/mol_type="genomic DNA"
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/mol_type="genomic
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OS Artificial Sequence
PN JP 2002272469-A/11
PD 24-SEP-2002
PF 19-MAR-2001 JP 2001079524
PI KAZUYUKI HIRATSUKA, NAOPUMI TAKASE, TOMOHIDE MAEDA PC C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Artifici sequence: primer sequence
FH Key Location/Qualifiers
FT source /organism='Artificial Sequence'.
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other sequences; artificial sequences.

1 (bases 1 to 30)

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1 Hiratsuka,K., Takase,N. and Maeda,T.

Cis-regulatory sequence exhibiting performace of regulating the expression of DNA damge-responsive gene of higher plants Patent: JP 200272469-A 11 24-SEP-2002;

PERSTURNT OF NARA INSTITUTE OF SCIENCE AND TECHNOLOGY
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Cis-regulatory sequence exhibiting performace of regulating the expression of DNA damge-responsive gene of higher plants Patent: JP 2002272469-A 16 24-SEP-2002;

PRESIDENT OF NARA INSTITUTE OF SCIENCE AND TECHNOLOGY

OS Artificial Sequence
PN JP 2002272469-A/16
PD 24-SEP-2002
PF 19-MAR-2001 JP 2001079524
PI KAZUYUKI HIRATSUKA, NAOPUMI TAKASE, TOMOHIDE MAEDA PC
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rosids; eutron.

E 1 (bases 1 to 44)

S Hiratsuka, K., Takase, N. and Maeda, T.

Cis-regulatory sequence exhibiting performace of regulating the expression of DNA damge-responsive gene of higher plants
Patent: JP 2002272469-A.1

PATENT OF NARA INSTITUTE OF SCIENCE AND TECHNOLOGY
OS Arabidopsis thaliana (thale cress)
PN JP 2002272469-A/1

PD 24-SEP-2002
PP 19-MAR-2001 JP 201079524
PI KAZUYUKI HIRATSUKA, NAOFUMI TAKASE, TOMOHIDE MAEDA PC
CI2N15/09, A0115/00, C12N5/10, C12N15/00, C12N5/00 CC Cis-regulatory
the
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Cis-regulatory sequence exhibiting
expression of DNA damge-responsive
                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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Paradigm Therapeutics Limited (GB)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Primer"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Pred. No. 1.4e+05;
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Pred. No. 1.5e+05;
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gene of higher plants.
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Sequence 363 from Patent
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CS136626.1 GI:72062239
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Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetic"
                                   /organism="synthetic construct"
/mol_type="unassigned RNA"
/mol_tyte="taxon:32630"
/moEe="Synthetic"
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AR403212
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BD166383
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Best Local S
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Nucleotide sequences specific to francisella
for the detection of francisella tularensis
Patent: WO 2004013357-A 31 12-FEB-2004;
The Regent of the University of California (U
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Chiron &
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Sequence 169 from Patent
AX236476
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Francisella tularensis
Bacteria; Proteobacteria;
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Heterologous expression of neisserial proteins
Patent: WO 0164922-A 169 07-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Francisella tularensis"
/mol_type="unassigned DNA"
/db_xref="taxon:263"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                           /organism="synthetic construct"
/mal_type="unassigned DNA"
/mal_type="taxon:32630"
/mbe="Oligonucleotide"
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                                                                                                                                                                                                                                                                                                                  GI:15796062
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85.0%;
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89.5%;
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Pred. No. 3.4e
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Pred. No. 6.4e+04;
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8: gb_pr:*
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 AR038929
AR038929
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AR121186
E36141
AR437559
AX0252600
BD190359
CQ5532663
BC19679846
AR35629050
AR537846
AR356290
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AR366012
AX149014
CQ6738874
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CC9778674
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AX1625619
AX825619
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AX33045 Arabidops
CQ537841 Sequence
AX485897 Sequence
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ED080955 Agonist
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AR183482 Sequence 10
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AR540638 Sequence
AX5109233 Sequence
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AR64099 Sequence
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US-10-310-914A-1285165/c
; Sequence 1285165, Application US/10310914A
; Publication No. US20060003322A1
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; OTHER INFORMATION: Synthetic
US-11-054-047-197
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TITLE OF INVENTION: RNA Interference Mediated Inhibition of TGF-Beta and TGF-Beta
TITLE OF INVENTION: Receptor Gene Expression Using Short Interfering Nucleic Acid
TITLE OF INVENTION: (sinA)
FILE REFERENCE: 400/248 (MBHB02-1193-E)
CURRENT TAPLICATION NUMBER: US/11/054,047
CURRENT FILING DATE: 205-02-09
NUMBER OF SEQ ID NOS: 855
SOFTWARE: PatentIn version 3.3
SEQ ID NO 197
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes;
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 1285165
LENGTH: 20
TYPE: NA
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APPLICANT: Guerciolini, Roberto
APPLICANT: Robin, Howard
APPLICANT: McSwiggen, James
                                                                                Matches
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Local Similarity 93.3%;
hes 14; Conservative
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                                                                                                Match 67.0%;
Local Similarity 93.3%;
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Pred. No. 1.5e+03;
                                                                              Score 13.4; DB 8;
Pred. No. 1.5e+03;
0; Mismatches 1;
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Search completed: March 2, 2006, 01:39:37 Job time: 498.333 secs

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RESULT 26
US-11-175-859-90816
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US-11-121-849-126576
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US-11-121-849-126576
            GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 126576
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 416798, Application US Publication No. US20050272080A1 GENERAL INFORMATION:
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR PILING DATE: 2004-05-03
PRIOR PILING DATE: 2004-05-03
SOFTWARB: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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REFERENCE: 3690.1
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                                                                                                                                                                                                                                                                                                            Similarity
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Similarity 80.0%;
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Pred. No. 1.3e+03;
0; Mismatches 4;
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Pred. No. 1
                of Human
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                Polymorphism
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detecta
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1019817
                                                                                                                          APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Guerciolini, Roberto
APPLICANT: Robin, Howard
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inh
TITLE OF INVENTION: Receptor Gene Expression Usi
TITLE OF INVENTION: (sinA)
FILE REFERENCE: 400/248 (MBHB02-1193-E)
CURRENT APPLICATION NUMBER: US/11/054,047
CURRENT FILING DATE: 2005-02-09
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US-10-310-914A-1019817
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                                                      NUMBER OF SEQ ID NOS: 855
SOFTWARE: PatentIn version 3.3
SEQ ID NO 69
LENGTH: 19
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Publication No. US20060003322A1
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Publication No. US20050287128A1
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PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
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CURRENT FILING DATE: 2005-07-05
                                      TYPE: RNA
ORGANISM: Artificial Sequence FEATURE:
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93.3%;
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Pred. No. 1.5e+03;
0; Mismatches 1;
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Pred. No. 1.6e+03;
0; Mismatches 4
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                                                                                                                                                                                                            Inhibition of TGF-Beta and TGF-Beta Using Short Interfering Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
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OTHER INFORMATION: Synthetic

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US-11-121-849-216448
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US-11-136-527-228156/c
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US-11-175-859-31164
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; ORGANISM: Homo sapien
US-11-121-849-216448
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT PILING DATE: 2005-05-03
PRIOR PILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 216448
LENGTH: 25
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                                                                                                                                                          Sequence 31164, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
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SEQ ID NO 228156
LENGTH: 25
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Best Local Similarity 88.2%;
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 352830
                                                                                    APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                      FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
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PRIOR APPLICATION NUMBER: US 60/585,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial
FEATURE:
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Pred. No. 1e+03;
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable gro
TITLE OF INVENTION: Bioinformatically detectable gro
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 16997
LENGTH: 76
TYPE: RNA
ORGANISM: Human
US-10-310-914A-16897
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US-11-121-849-98438/c
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Best Local Similarity
**-*-hes 9; Conserve
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                                                                       ; ORGANISM: Homo sapien US-11-121-849-98438
                                                                                                                                                                                                                                                                                                                            Sequence 98438, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
                                                                                                        NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 98438
LENGTH: 25
TYPE: DNA
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 Matches
               Query Match
Best Local Similarity
                                                                                                                                                                                             TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REPERENCE: 3684.1 CURRENT APPLICATION NUMBER: US/11/121,849 CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR FILING DATE: 2004-05-03 PRIOR FILING DATE: 2004-05-03 PRIOR FILING DATE: 2004-05-03
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NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3
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TYPE: DNA
ORGANISM: homo sapien
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78.9%;
                 68.0%;
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Pred. No. 1.2e+03;
1; Mismatches 3
                 Score 13.6;
Pred. No. 1.
0; Mismatches
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                   1.3e+03;
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                                    DB 12;
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   Indels
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; ORGANISM: Human
US-10-310-914A-318333
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US-10-310-914A-318333/c
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; ORGANISM: Homo sapiens
US-11-083-784-1224663
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APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes of the provided in the state of the stat
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 97395
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local
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Best Local Similarity 100.0%;
Matches 14; Conservative 0;
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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SOFTWARE: Proprietary
SEQ ID NO 1224663
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PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-14
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100.0%; Pr
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%; Pred. No. 7.3
0; Mismatches
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7.8e+02;
hes 0; Indels
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hes 0;
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US-11-121-849-160639
                                                                                                                         ; ORGANISM: Homo sapien US-11-121-849-160639
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US-10-310-914A-751272
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                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 160639
                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: John Palma
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                                                              Matches
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Best Local :
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APPLICANT: Shiler, Kruzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1
                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
                                                                                                                                                                          LENGTH: 25
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                   1 TCCCCATATTTATGGAA 17
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88.2%;
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Pred. No. 9.7e+02;
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Pred. No. 16
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Pred. No. 9.5e+02;
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US-11-101-244-222605
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                                                                                                                                                                                                            RESULT 12
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Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 606251 LENGTH: 25
                                                                                                                               Sequence 1224663, Application US/11101244 Publication No. US20050246794A1 GENERAL INFORMATION:
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-11-121-849-606251
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
                                                                        APPLICANT:
                                                                                                              APPLICANT: Dharmacon, Inc
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1591911
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Similarity 100.0%; Pred. No.
14; Conservative 0; Mismatc
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                                                                        Khvorova, Anastasia
Reynolds, Angela
                                                           Leake, Devin
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84.2%;
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Pred. No. 6.2e+02;
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Sequence 1224663, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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SEQ ID NO 1224663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
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APPLICANT: Khvorova,
APPLICANT: Reynolds,
APPLICANT: Leake, Dev
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Homo sapiens
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Reynolds, Angela
Leake, Devin
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Scaringe, Stephen
                                                                                                                                                                                                                                                         70.0%; Score 14; DB 11; ilarity 100.0%; Pred. No. 7.3e+03 Conservative 0; Mismatches
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APPLICANT:

APPLICANT:

Khvorova, Anastasia Reynolds, Angela Leake, Devin Marshall, William Scaringe, Stephen

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; ORGANISM: homo sapien US-11-175-859-111867
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US-10-310-914A-113805
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                                                                                                                                                                                                                                                                                                                           Sequence 111867, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
TILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 113805
                                                                                                                      SEQ ID NO 111867
LENGTH: 50
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     Matches
                                   Query Match
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Best Local
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Best Local
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
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CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 22
TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 22
TYPE: RNA
ORGANISM: Human
                 Local Similarity
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es 11; Conservative
     16;
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   Conservative
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88.9%;
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61.1%;
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 Score 14.8; DB 12;
Pred. No. 3.6e+02;
0; Mismatches 2;
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Pred. No. 2.8e+02;
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Pred. No. 2.8e+02
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                               DB 12;
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                                 Length 50;
   Indels
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RESULT 10
US-11-121-849-606251
; Sequence 606251, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: Probe
US-11-136-527-194511
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; ORGANISM: Homo sapien
US-11-121-849-165142
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US-11-121-849-165142
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Best Local Similarity
Matches 15; Conserv
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CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 194511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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SOPTWARE: Microarray Probe Sequence Listing Generator
SEQ ID NO 165142
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling
FILE REFERENCE: 031896-041000 (AM101086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
PRIOR FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                   LENGTH:
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93.8%;
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93.8%;
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Pred. No. 4.8e+02;
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Pred. No. 4.
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GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION SERVICES OF SERVIC
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US-11-175-859-5611/c
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US-11-175-859-92965
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Best Local S
Matches 17
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Liu, Guoying et al.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
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25
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                                                                                                ch 76.0%;
1 Similarity 85.0%;
17; Conservative
                             1 TCCCCATATTTATGGAATGA 20
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64.0
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US-10-310-914A-30159
US-10-750-185-18779
US-10-750-623-18779
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US-11-121-849-216447
US-11-121-849-355721
                                                                                                                           Score 15.2;
Pred. No. 2
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Sequence 30159, A
Sequence 18779, A
Sequence 18779, A
Sequence 69880, A
Sequence 216447,
Sequence 315721,
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RESULT 3

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RESULT 5
US-10-310-914A-113804
; Sequence 113804, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detection.
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US-10-310-914A-113803
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; TYPE: DNA
; ORGANISM: Eucalyptus
US-11-024-959-556
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 113803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT FILING DATE: 2004-12-30
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR FILING DATE: 2003-12-30
NUMBER OF SEQ ID NOS: 782
SOPTWARE: Patentin version 3.3
SEQ ID NO 556
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Best Local (
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Best Local Similarity 85.0%;
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APPLICANT:
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APPLICANT: CONNETT, WARIE B.
APPLICANT: EMERSON, SAAH JANE
APPLICANT: GRIGGR, MURRAY ROBERT
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: LUND, STEVEN TROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: RNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 22
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                                                                                                                                                                                                                                                                                                        Similarity
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Pred. No. 2.3e+02;
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Pred. No. 2.8e+02;
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1: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq1:*
7: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq1:*
8: /cgn2_6/ptodata/1/pubpna/USI0_NEW_PUB.seq1:*
9: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq2:*
10: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq3:*
13: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq4:*
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US-10-310-914A-113804

US-10-310-914A-113805

US-10-310-914A-113805

2 US-11-175-859-111867

2 US-11-121-849-165142

2 US-11-121-849-166251

2 US-11-121-849-22605

US-11-121-849-22605

US-11-101-244-222605

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Sequence 1224663,
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2 US-11-125-859-90816
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US-10-310-914A-1285165
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Sequence 31164, A
Sequence 1887, A
Sequence 19813, A
Sequence 98413, A
Sequence 90116, A
Sequence 1019817, S
Sequence 1074096, Sequence 1977, Appl
Sequence 1174096, Sequence 21556, A
Sequence 21556, A
Sequence 105470, Appl
Sequence 10556, Appl
Sequence 10556, Appl
Sequence 105697, Appl
Sequence 10700, Appl
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RESULT 26
US-10-719-900-775584
; Sequence 775584, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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US-10-719-900-958681
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US-10-719-900-357261
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LENGTH: 25
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Best Local
           APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
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APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

PRIOR FILING DATE: 2002 11
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
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TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3528.1
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SOFTWARE: Microarray Probe Se
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NUMBER OF
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ORGANISM: Mus musculus
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Pred. No. 1.3e+04;
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; ORGANISM: Probe Sequence
US-10-956-157-90813
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US-10-956-157-90813/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wyeth
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 90813
LENGTH: 251
TYPE: NOT
                                                                                                                                                                                                                                                                                                                                                  Sequence 146740, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
                                                                             Best
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SOFTWARE: PATENTIN version 3.2
SEQ ID NO 146740
LENGTH: 25
                                                                                            Query Match
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APPLICANT: MOUNTS, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WI
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
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Pred. No. 1.3e+04;
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RESULT 20
US-10-786-720-7426/c
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US-10-786-720-9676/c
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; ORGANISM: Homo sapiens
US-10-786-720-7426
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; ORGANISM: Homo sapiens
US-10-786-720-9676
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
SOFTWARE: PAtentIn version 3.2
SEQ ID NO 7426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7426, Application US/10786720 Publication No. US20040191818A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9676, Application US/10786720 Publication No. US20040191818A1 GENERAL INFORMATION:
                                                                         Sequence 4223, Application US/10098263B Publication No. US20030104410Al GENERAL INFORMATION:
APPLICANT: Miteman, Michael TITLE OF INVENTION: Human Microarray FILE REFERENCE: 3118.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2
SEQ ID NO 9676
LENGTH: 21
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Best Local :
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APPLICANT: O'Toole, Margot
APPLICANT: Liu, Wei
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/786,720
CURRENT FILING DATE: 2004-02-26
NUMBER OF SEQ ID NOS: 21135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
TITLE OF INVENTION: DISEASES
FILE REFERENCE: 031896-023000 (AM101331L)
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APPLICANT: O'Toole, Margot
APPLICANT: Liu, Wei
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1 Similarity 88.2%;
15; Conservation
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US-10-719-956-234869
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                                                                                                                               ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-399696
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 234869
LENGTH: 25
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
FILE REFERENCE: 3527.1
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 607427,836
PRIOR APPLICATION NUMBER: 607427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 399696
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Best Local S
Matches 15
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 4223
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Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3527.1
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                                CCCATATTTATGGAATG 19
                                                               Conservative
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88.2%;
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                                                                 Score 13.8; DB Pred. No. 1.3e+(0; Mismatches
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Pred. No. 1.3e+04;
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APPLICANT: Susan Gregory
TITLE OF INVENTION: MOUSE MODEL FOR BONE METABOLISM
FILE REFERENCE: 23546-8149/BIOL0019US
CURRENT APPLICATION NUMBER: US/10/667,236
CURRENT FILING DATE: 2003-09-17
NUMBER OF SEQ ID NOS: 358
SEQ ID NO 349
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wyeth
APPLICANT: Mounts, William
APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 313397
LENGTH: 25
TYPE: DNA
TYPE: DNA
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Publication No. US20050118625A1
GENERAL INFORMATION:
SEQ ID NO 349
                                                                                                                                                                                                                                                                     Publication No.
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                              APPLICANT: Joshua Finger
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: MODULATION OF RANKL EXPRESSION
FILE REFERENCE: 23546-08148/RTS-0618US
CURRENT APPLICATION NUMBER: US/10/944,274
CURRENT FILING DATE: 2004-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                       APPLICANT: Brenda F. Baker
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
APPLICANT: Kathleen Myers
APPLICANT: Joshua Finger
                   NUMBER OF SEQ ID NOS:
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1 Similarity 84.2%;
16; Conservation
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16; Conservative
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o. US20050148533A1
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84.2%;
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Pred. No. 8.6e+03;
0; Mismatches 3;
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Pred. No. 8.6e+03;
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US-10-719-900-75079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; Mus musculus US-11-036-317-127081
                                                                                                      US-10-719-900-75079
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Sequence 127081, Application US/11036317
Publication No. US20050214823A1
GENERAL INFORMATION:
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                                                                                                                                               FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER: OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 75079
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 127081

LENGTH: 25
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Matches
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Best Local Similarity
Matches 16; Conserv
                                      Matches
                                                                     Query Match
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                                                                                                                                                                                                                                                                                                     APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, Alan
APPLICANT: Blume, John
                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
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ORGANISM: Artificial Sequence
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16; Conserv
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                                                   Similarity
   ATATTTATGGAATG 19
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                                    Conservative
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84.2%;
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                                                  70.0%; Score 14; DB 8; L
100.0%; Pred. No. 1.1e+04;
                                    0,
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Pred. No. 8.6e+03;
0; Mismatches 3
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Pred. No. 8.6e+03;
0; Mismatches 3
                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                 Length 25;
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                                Gaps
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Sequence 442498, Application US/10719956 Publication No. US20040146910A1

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Sequence 594991, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 599466
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                                                                                                                                                                                                                                                                                                         RESULT 12
US-11-036-317-612570/c
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US-10-719-956-594991/c
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; ORGANISM: Rattus norvegicus
US-10-719-956-594991
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 442498
FERCENT COLUMN ACCESSION NUMBER: COLUMN ACCESSION NO 4242498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
                                                                                                                                                                                                                                            Sequence 612570, Application US/11036317 Publication No. US20050214823A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 594991
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NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 612570
LENGTH: 25
                                                           APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2005-01-13
PRIOR FILING DATE: 2005-01-13
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93.8%;
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93.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.4; DB 7;
Pred. No. 6.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou

ITILE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 328.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER: OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 632106

LENGTH: 25
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US-10-719-900-379430/c
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Best Local Similarity
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Best Local
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                                                                                    Query Match
Best Local (
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 25
                                                          71.0%;
Local Similarity 84.2%;
les 16; Conservarion
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Local Similarity 84.2%;
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                                  1 TCCCCATATTTATGGAATG 19
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 TCAACATATTTATGGAGTG 24
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93.8%;
                                                                                                                                                                                                                              Sequence Listing Generator V 1.1
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Pred. No. 6.9e+03;
                                                                                      Score 14.2; DB 8;
Pred. No. 8.6e+03;
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Pred. No. 8.6e+03
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                                                                                                        Length 25;
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RESULT 15 US-10-667-236-349/c

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APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
TITLE OF INVENTION: SOLUBLE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0242
CURRENT APPLICATION NUMBER: US/10/672,866
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/633,843
PRIOR APPLICATION NUMBER: 09/888,360
PRIOR APPLICATION NUMBER: 09/888,360
PRIOR PILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 339
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                                                                                                                           ; OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-866-269
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US-10-719-900-705399
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                                                            Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 269, Appublication No.
                                                                                                                                                                                                         SEQ ID NO 269
LENGTH: 20
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Best Local Similarity
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SCPTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
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Similarity 88.9%;
                                                                           Similarity
                            TCCCCATATTTATGGA 16
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                                                                           72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.0%;
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Pred. No. 4.5e
0; Mismatches
                                                            0
                                                                         Score 14.4; DB 8;
Pred. No. 6.7e+03;
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Pred. No. 7.7e+02;
0; Mismatches 1
                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5e+03;
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                                                                                        Length 20;
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                                                        Gaps
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APPLICANT: Kenneth Dobie
ITITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
ITITLE OF INVENTION: SOLUBLE
ITITLE OF INVENTION: SOLUBLE
ITITLE OF INVENTION: EXPRESSION
FILL REFERENCE: RTS-0242
CURRENT APPLICATION NUMBER: US/10/672,866
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/633,843
PRIOR APPLICATION NUMBER: 10/633,843
PRIOR APPLICATION NUMBER: 10/633,843
PRIOR APPLICATION NUMBER: 09/88
PRIOR APPLICATION NUMBER: 09/88
PRIOR FILING DATE: 2003-08-04
PRIOR FILING DATE: 2001-06-21
NUMBER: OF SEQ ID NOS: 339
LENGTH: 20
TYPE: DIA
CREATION ALLEGICAL GROUPS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/888,360
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 339
SEQ ID NO 271
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: C. Frank Bennett
APPLICANT: Kenneth Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
TITLE OF INVENTION: SOLUBLE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0242
CURRENT FILINGION NUMBER: US/10/672,866
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/633,843
PRIOR FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-04
PRIOR FILING DATE: 2003-08-04
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APPLICANT: Kenneth Dobie
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                         LENGTH: 20
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                                                                                                     Similarity
TCCCCATATTGATGGA 20
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Pred. No. 6.7e+03;
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Pred. No. 6.7e+03;
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RESULT 10 US-10-719-956-442498

Sequence 589091,

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RESULT 1
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US-10-173-192-37
Sequence 37, Application US/10173192
Publication No. US20030236204A1
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US-10-173-192-62/c
; Sequence 62, Application US/10173192
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                         RESULT 3
US-10-653-528-37
; Sequence 37, Application US/10653528
; Publication No. US20040077578A1
; GENERAL INFORMATION:
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SEQ ID NO 37
LENGTH: 20
TYPE
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APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Do
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SEQ ID NO 62
LENGTH: 20
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/173,192
CURRENT FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION FILE REFERENCE: PTS-0022
CURRENT APPLICATION NUMBER: US/10/173,192
CURRENT FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kenneth W. Dobie TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
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APPLICANT: Brett P
APPLICANT: Kenneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                           ORGANISM: H. sapiens FEATURE:
                                                                                                                                                                                                                                                                                        TYPE: DNA
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Local Similarity 100.0%; Pred. No.
les 20; Conservative 0; Mismatch
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Brett P. Monia
Kenneth W. Dobie
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US-10-891-260-4570
US-10-057-890A-27
US-11-010-397-27
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Sequence 27, Appl
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US-10-719-900-705398
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-705398
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CURRENT APPLICATION NUMBER: US/10/653,528
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR PRIOR PRIOR OF SEQ ID NOS: 71
SEQ ID NO 37
SEQ ID NO 37
                                                                                                                                                                                                                                                                       ; Sequence 705398, Application US/10719900 ; Publication No. US20050026164A1
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                                                                                                      GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR APPLICATION NUMBER: 61/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/653,528
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 62
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Best Local Similarity
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APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: PTS-0022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: H. FEATURE:
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-672-866-270

US-10-672-866-271

US-10-719-956-442498

US-10-719-956-594991

US-11-036-317-612570

US-11-036-317-612570

US-10-719-900-632106

US-10-956-157-313397

US-10-944-274-349

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US-10-967-236-349

US-10-967-236-349

US-10-968-236-349

US-10-968-236-349

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US-10-786-720-9676
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 Sequence 820, Appl Sequence 26954, Appl Sequence 26954, Appl Sequence 26954, Appl Sequence 27501, App Sequence 580372, App Sequence 580372, App Sequence 580374, App Sequence 595455, Appl Sequence 595455, Sequence 595455, Sequence 595455, Appl Sequence 595455, Sequence 595455, Sequence 595455, Sequence 595455, Sequence 595455, Appl Sequence 11261, Appli Sequence 11261, Appli Sequence 11, Appli Sequence 11455, App Sequence 11455, App Sequence 11455, App Sequence 11555, App Sequence 555, App Sequence 5526, App Sequence 55262, App Sequence 55260, Appli Sequence 55262, App Sequence 55260, App Sequence 55260, Appli Sequence 55260,
                                                                                                                                                                                                                                                                            Sequence 958681,
Sequence 90813, A
Sequence 146740,
Sequence 268246,
Sequence 377588,
Sequence 6318, A
Sequence 92572, A
Sequence 145605,
Sequence 208327,
Sequence 208327,
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Sequence
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357261,
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; MOLECULE TYPE: DNA (genomic)
US-08-557-210A-21
                                                                                                                                                                                                                                                                                                                                                                                                 US-10-131-827-3955
                                                                                                                                                                                                                                                                                                     Sequence 3955, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                           APPLICANT: EY, KIRK
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, Nor
APPLICANT: Woodward, Nor
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                         NUMBER OF SEQ ID NOS: 9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 040433/0142/SOPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dorner, Friedrich TITLE OF INVENTION: An expression plasmid, a fusion protein, a TITLE OF INVENTION: transfected eukaryotic cell line, a method of producing forei TITLE OF INVENTION: proteins, a foreign protein preparation as well as a pharmace TITLE OF INVENTION: composition

NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: A 2099/94 FILING DATE: 14-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: (FILING DATE: 14-NOV-: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STREET: 3
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3000 K Street, N.W., Suite
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Falkner, Falko Guenther
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87.5%;
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Pred. No. 4.4e+03;
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; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-3955
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US-09-198-452A-4383
                                                                                                                                                                                                                             APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
ITILE OF INVENTION: Biallelic markers for use in
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER APPLICATION NUMBER: US 60/082,614
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APPLICANT: Griffals, R.
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3955
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Patent No. 6559294
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Best Local Similarity 87.5%;
Matches 14; Conservative
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SEQ ID NO 10736
LENGTH: 21
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Query Match
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CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 20
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                              FEATURE:
                                                          LOCATION: 1..21
OTHER INFORMATION: downstream
                                                                                                                                                         TYPE: DNA
                                                                                                                                   ORGANISM:
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1 Similarity 78.9%;
15; Conservation
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                                                                                          primer_bind
                                                                                                                                     Homo Sapiens
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    63.0%;
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Pred. No. 5.1e+03;
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Pred. No. 4
    Score 12.6;
                                                          amplification primer 99-19544 for
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  Length 21;
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                                                              SEQ 2871,
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                                                                                                                                  PILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/427,
APPLICATION NUMBER: US 07/427,
PILING DATE: 27-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: LOGAN, April C.
REGISTRATION NUMBER: 33,950
REFERENCE, DOCKET NUMBER: 184.:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (619) 554-237
                                                                                   TELEFAX: (619) 554-6312 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/491,322
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hein, Mich B.
APPLICANT: Hiatt, Andrew C.
APPLICANT: Ma, Julian K.C.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING
TITLE OF INVENTION: SECRETORY ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TOPOLOGY: 1:
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                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                  ENGTH:
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REGISTRATION NUMBER: 34,61
REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (619) 552-0159
                         nucleic acid
nucleic single
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California
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Similarity 87.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                  31 base pairs
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10666 No. 6852319th Torrey Pines Road, TPC-8
                  linear
DNA (genomic)
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Pred. No. 4.
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RESULT 27
US-08-557-210A-21
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; ANTI-SENSE: 1
US-09-491-322-13
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US-08-100-118-12/c
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                                                                                                                                       Best
                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Strodthoff, Kristine M.
REGISTRATION NUMBER: 34,259
REFERENCE/DOCKET NUMBER: 8682
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Design, Construction and Express
TITLE OF INVENTION: of Chimeric Proteins for Develop
TITLE OF INVENTION: Vaccines and Diagnostic Reagents
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kang, Chil-Y
APPLICANT: Luo, Lizhong
                                                                                                                                                                                                                                                         LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                       Local
                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: UPFILING DATE: 19930730 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 87.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5580773west Center
                                                              23
                                                                                           3 CCCATATTTATGGAAT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55402
                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minneapolis
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                                                                                                                                                                                                                                                                                                                                      612-332-9081
                                                                                                                          Conservative
                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.0%;
87.5%;
                                                                                                                                       64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Design, Construction and Expression of Chimeric Proteins for Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/100,118
                                                                                                                                                                                                                                                                                                                                                                                  8682.6-US-01
                                                                                                                    Score 12.8; DB 2;
Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Pred. No. 4.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
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                                                                                                                                                   Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 31;
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                                                                                                                       Gaps
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Sequence 21, Application US/08557210A Patent No. 6114146 GENERAL INFORMATION:

APPLICANT:

Herlitschka, Sabine

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RESULT 23
US-09-199-534-13
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                                                                                                                                                                                                                                                                                                            Sequence 13, Application Patent No. 6417429
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/427,765
FILING DATE: 27-OCT-1989
ATTORNBY/AGENT INFORMATION:
NAME: LOGAN, APTI1 C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 184.2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 64.0%;
Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 1066 No. 6329569th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COUNTRY: US
ZID: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                    NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCR
                                                                                                                                                                                                          Ma, Julian K.C.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
SECRETORY ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                        APPLICANT: Hein, Mich B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CCATATTTATGGAATG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/199,534
FILING DATE: 25-No. 6329569-1998
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: La Jolla
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGATCTATGGAATG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/642,406 FILING DATE: <Unknown>
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                                                                                              CITY: La Jolla
STATE: California
                                                                                                                                  ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE STREET: 10666 No. 6417429th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                  Application US/09199534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <Unknown>
27-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Pred. No. 4.3e+03;
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Best Local
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Sequence 15, Application US/09717888
Patent No. 6808709
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: 184.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,406
APPLICATION UNBER: 08/642,406
APPLICATION UNBER: US 07/427,765
FILING DATE: 27-CCT-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/09/199.534
FILING DATE: 25-No. 6417429-1998
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                               ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM PC:
SOFTWARE: WOTCH PETFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 13:
APPLICATION NUMBER: 08/367,395 FILING DATE: 30-Dec-94 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                         APPLICATION NUMBER: US/09/717,888 FILING DATE: 20-No. 6808709-2000 CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGATCTATGGAATG 17
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                                                           APPLICATION NUMBER: US/08/434,000 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 633 West Fifth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
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                                                                                                                                                                                                                                                                                                                                                                                                                             Suite 4700
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87.5%;
                                                                                                                                                                                                                                                                             storage
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Pred. No. 4.3e+03;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                   1.44 Mb
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US-08-434-000A-15
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US-08-434-000A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Apr. No. 604603
   Matches
                 Best Local Similarity
                                 Query Match
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                                                                                                                                        TELEX: SEQUENCE LISTING INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA: includi:
PRIOR APPLICATION DATA: describ.
PRIOR APPLICATION DATA: describ.
APPLICATION NUMBER: 08/367,39

FILING DATE: 12/30/94

ATTORNEY AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613

REFERENCE/DOCKET NUMBER: 212/
TELEPHONE: (619) 552-8400

TELEPHONE: (619) 552-0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANDREW C. HIATT, JULIAN
APPLICANT: K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOCLOBILINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: I
                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                        TELEX: 67-3510
                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
   14;
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: California
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                                                                                                                         31 base pairs
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633 West Fifth Street
Suite 4700
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
                                                                                linear
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                64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                            1: including application
1: described below:
08/367,395
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Score 12.8; DB 3;
Pred. No. 4.3e+03;
0; Mismatches 2;
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Pred. No. 4.3e+03;
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                            Length 31;
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RESULT 22
US-09-199-534-13
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TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-312-157-15
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US-09-312-157-15
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                                                   Sequence 13, Application US/09199534
Patent No. 6329569
GENERAL INFORMATION:
APPLICANT: Hein, Mich B.
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE LISTING INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Guise, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/312,157
FILING DATE: 14-May-199
CLASSIFICATION: CUnknown>
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,000
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                     CCAGATCTATGGAATG 17
                                                                                                                                                                                                                           CCATATTTATGGAATG 19
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09312157
                                                                                                                                                                                                                                                                           Conservative
                 Hiatt, Andrew C. Ma, Julian K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 4700
                                                                                                                                                                                                                                                                                            64.0%;
87.5%;
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Pred. No. 4.3e+03;
0; Mismatches 2
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US-10-057-890A-27/c
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US-09-396-196G-37968
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                                                                                                                                   ; ORGANISM: Mus musculus 
US-09-396-196G-37968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Synthetic oligonucleotides used to join DNA fragments US-10-057-890A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Coleman, Timothy
APPLICANT: Honefield, Brian
TITLE OF INVENTION: Scaffold Fusion Polypeptides, Composition for Making the Same,
TITLE OF INVENTION: of Using the Same.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/265,858
PRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 27
LENGTH: 42
                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37968
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37968, Application US/09396196G Patent No. 6821724
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                                                                     Matches
                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                            APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT SPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Michael Mittmann APPLICANT: David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/057,890A
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: 60/265,782
PRIOR FILING DATE: 2001-01-31
PRIOR PRIOR DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                    ENGTH: 25
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les 13; Conserv
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                                                                                   Similarity
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                                  TCCCCATATTTATGGA 16
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   TCCCCANATTTCTGGA 24
                                                                     Conservative
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87.5%;
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1; Mismatches 4
                                                                Score 12.8; DB 3;
Pred. No. 4.2e+03;
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Pred. No.
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RESULT 18
US-09-396-196G-120208/c
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Best Local S
Matches 14
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SEQ ID NO 120208
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 120208, F
Patent No. 6821724
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Michael Mittmann APPLICANT: David Mack
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/642,406A
FILING DATE: 03-MAY-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hein, Mich B.
APPLICANT: Hiatt, Andrew C.
APPLICANT: Ma, Julian K.C.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ASSEMBLED
TITLE OF INVENTION: SECRETORY ANTIBODIES
                                                  APPLICATION NUMBER: US 0: FILING DATE: 27-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,
                                                                                                                                             APPLICATION NUMBER: US 07/591,823
FILING DATE: 02-OCT-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 554-2937
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                      REFERENCE/DOCKET NUMBER:
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David Lockhart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                  33,950
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Pred. No. 4.2e
0; Mismatches
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APPLICANT: Segawa, Toshiaki
TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
FILE REFERENCE: 06501-021001
CURRENT APPLICATION NUMBER: US/09/142,956B
CURRENT FILING DATE: 1999-03-04
PRIOR APPLICATION NUMBER: PCT/JP98/00140
PRIOR APPLICATION NUMBER: PCT/JP98/00140
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-01-17
NUMBER OF SEQ ID NOS: 14
SCETWARE: East SEC FOR Windows Version 40
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                                                                       Matches
                                                                                                         Query Match
                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                          Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LO, KATHORINE C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS AND FILE REFERENCE: FC-3-C1-1
CURRENT APPLICATION NUMBER: US/09/634,530
CURRENT APPLICATION NUMBER: 09/471,528
PRIOR APPLICATION NUMBER: 09/471,528
PRIOR APPLICATION NUMBER: 09/182,816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Niwa, Mikio APPLICANT: Okamoto, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 089;
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                    FEATURE: OTHER INFORMATION: Synthetically generated primer
                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
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                                                                                                                                                                                                                                    ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 38
                                                                                        Local
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25
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                      1 TCCCCATATTTATGGAAT 18
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15; Conserva
                                                                                      Similarity
TCTCCATATTATAGGAT 8
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Silver, Gary M.
Lo, Katherine C.
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                                                                     Conservative
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                                                                                    Score 13.2; DB 3;
Pred. No. 2.8e+03;
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Pred. No. 2.
                                                                     Mismatches
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                                                                                                     DB 3;
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                                                                     Indels
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US-09-326-806-4/c
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US-09-422-978-723
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SOFTWARE: PatentIn Ver. :
SEQ ID NO 4
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GENERAL INFORMATION:
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SEQ ID NO 723
    Query Match
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Patent No. 6537751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ovadis, Marianna
APPLICANT: Itzhaki, Hanan
TITLE OF INVENTION: Carotenoid-Associated Proteins Useful For High
TITLE OF INVENTION: Carotenoid Accumulation And Production In Plants And
TITLE OF INVENTION: Other Organisms
                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 59458
CURRENT APPLICATION NUMBER: US/09/326,806A
CURRENT FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: PCT/IL97/00399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Vainstein, Alexander APPLICANT: Vishnevetsky, Michael
                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: 60/032,421
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CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET 020CP1
                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1996-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1998-04-21
                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: syntheitic OTHER INFORMATION: oligonucleotide
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NAME/KEY: allele
                                                                   OTHER INFORMATION: n = inosine
                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 24
OTHER INFORMATION: 99-16847-405 : polymorphic base
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                                                                                               FEATURE:
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nes 15; Conserv
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    65.0%; Score 13;
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Pred. No. 2
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Length 24;
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PRIOR FILING DATE: 1998-09-17

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Best Local Similarity
Matches 15; Conserve
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US-09-396-196G-118553
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 118553
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                                                               Matches
                                                                                              Query Match
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                                                                                                                                                                                                                                             TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/989,510A
PILING DATE: 12-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WISNEWSKI, NANCY
APPLICANT: SILVER, Gary M.
APPLICANT: LO, Katherine Cailles
APPLICANT: BRANDT, Kevin S.
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 38 nucleotides
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
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                                                                                                                                              MOLECULE TYPE; Primer
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                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                            STRANDEDNESS:
                                                                                Local
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5. 6037160
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                                                                                Similarity
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 TACCCATATTTATAGGAT
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milarity 83.3%;
Conservative
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                                                                 Conservative
                                                                                                                                                               linear
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                                                                                                                                                                            single
                                                                              66.0%; Score 13.2; DB 3;
83.3%; Pred. No. 2.8e+03;
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Pred. No. 2.6e.
0; Mismatches
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                                                                  Mismatches
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; LENGTH: 38
; TYPE: DNA
; ORGANISM: Artificial Sequence
; ORGANISM: HISTORIATION: Description
; OTHER INFORMATION: Primer
US-09-471-528-17
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US-09-471-528-17/c
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-182-816-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/09471528 Patent No. 6153397
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                                                                                       Query Match
Best Local Similarity
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                                                                        Matches
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APPLICANT: Brandt, Kevin S.

APPLICANT: Brandt, Kevin S.

APPLICANT: Brandt, Kevin S.

TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,

TITLE OF INVENTION: PROTEINS AND USES THEREOF

FILE REFERENCE: FC-3-C1

CURRENT APPLICATION NUMBER: US/09/182,816

CURRENT FILING DATE: 1998-10-29

EARLIER FILING DATE: 1997-12-12

RUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/471,528
CURRENT FILING DATE: 1999-12-27
EARLIER APPLICATION NUMBER: 09/182,816
EARLIER FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/889,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wisnewski, Nancy
APPLICANT: Silver, Gary M.
APPLICANT: Lo, Katherine C.
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FLEA EPOXIDE HYDROLASE PROTEINS
FILE REFERENCE: FC-3-C1-1
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TYPE: DNA
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Similarity 83.3%;
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TACCCATATTTATAGGAT 6
                       TCCCCATATTTATGGAAT 18
                                                                        Conservative
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                                                                                                                                                                 Description of Artificial Sequence: Primer
                                                                                         66.0%;
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Pred. No. 2.8e+03
                                                                        Score 13.2; DB 3
Pred. No. 2.8e+03,
0; Mismatches
                                                                                                             DB 3;
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RESULT 6

US-09-396-196G-66317

; Sequence 66317, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:
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Best Local S
Matches 15
                                                                                                                                                               Matches
                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45,
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arcd067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 321 No
                                                                                                                                                                             Local
                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                               ENGTH:
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                                                                                                                           1 TCCCCATATTTATGGAAT 18
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                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 No. 5773583th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                        (312) 245-4961
                                                                                                                                                              Conservative
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METHODS AND MATERIALS RELATING TO THE
FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
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                                                                                                                                                                          Score 13.2; DB 2;
Pred. No. 2.6e+03;
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Pred. No. 2.6e+03
                                                                                                                                                              Mismatches
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FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111261
LENGTH: 25
TYPE: DNA
OFFANTION TO SECURE STATES OF SECURE SEC
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CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 66317

LENGTH: 25
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Patent No. 6821724
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GENERAL INFORMATION:
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                                                                                                 APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
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ORGANISM: mus musculus
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Local Similarity 83.3%;
les 15; Conservative
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15; Conserv
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Pred. No. 2.6e+03;
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US-09-396-196G-66318
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OTHER INFORMATION: 12-640-325 : polymorphic base T or US-09-671-317-855
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LENGTH: 25
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Patent No. 6821724
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86
                                                                                                                                       SOFTWARE: PA
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                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
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TITLE OF INVENTION: Methods of Genetic Analysis
                           FEATURE:
NAME/KEY: allele
LOCATION: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Michael Mittmann APPLICANT: David Mack
                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
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                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                    LENGTH: 47
                                                                                  ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Chumakov, 11ya
PPLICANT: Bougueleret, Lydie
PPLICANT: Bougueleret, Lydie
PPLICANT: Cohen, Annick
ITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
ILE REFERENCE: 62.US3.CIP
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David Lockhart
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US-09-099-011A-37
US-09-098-877B-37
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Pred. No. 1.
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L.7e+03;
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Patent No.
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SEQ ID NO 56
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/09/467,642
CURRENT FILING DATE: 1999-12-20
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APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
                                    REFERENCE/DOCKET NUMBER: 36,111
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sukhatme, TITLE OF INVENTION: 1
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STATE: Illinois
                                                                             NAME: Coughlin, Daniel REGISTRATION NUMBER: 36
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321 No. 5763209th Clark Street, Suite 800
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METHODS AND MATERIALS RELATING TO THE FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
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US-09-258-367-27
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Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 13.2; DB 10; 83.3%; Pred. No. 1.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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         Search completed: March
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                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                 Local
                                                                             33 TCCCCATATTCAGAGAAT 16
                                                                                                                                                                         15; Conservative
                                                                                                                        1 TCCCCATATTTATGGAAT 18
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                        /dev_stage="13 day embryos"
/dev_stage="13 day embryos"
/lab host="SOUR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/corl; Site_2: XhoI; Cloned unidirectionally. Primer
Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCTTTTTTTTTTTTTT 3'"
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
/strain="NIH Swiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:1224419"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="pooled"
2,
                                                                                                                                                                                          66.0%;
83.3%;
       2006, 01:14:40
                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                 Score 13.2; DB 1;
Pred. No. 1.1e+05;
                                                                                                                                                                           Mismatches
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RESULT 28
AG194254
LOCUS
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AUTHORS
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KEYWORDS
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ACCESSION
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PUBMED
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                    20
              AG194254 31 bp DNA linear GSS 06 Pan troglodytes DNA, clone: RP43-072D07.TJ, genomic survey sequence.
                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A., Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L., Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W., Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C., Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M.L. and Margolis, J. A. complementary transposon tool kit for Drosophila melanogaster
AG194254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The piggyBac insertion position is 28 in the 31 bases. This insertion position refers to the first base of the 4 base TTAA target recognition sequence. Class: transposon insertion site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CZ469014.1 GI:62963027
GSS.
                                                                                                                                                                                                                                                                                                  Similarity
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Genet. 36 (3), 2
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Exelixis piggyBac PB insertions"
/note="Vector: piggyBac PB (GenBank accession number AY515146); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the PB element using Hsp70:piggyBac transposase from a single ammunition element on either the X or third chromosome. We induced transposase expression by immersing bottles in a circulating 37oC water bath for a daily (days 3-10 after egg-laying) 1-h heat shock. We outcrossed the resulting dysgenic males to an isogenic w- strain. New insertions were identified on the basis of a change in eye color (third chromosome ammunition) or the appearance of w+ male
                                                                                                                                                                                                                                                                                                                                                                                                          progeny (X chromosome ammunition). All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking
                                                                                                                                                                                                                                                                                                                                                                                           genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="isogenic w- strain"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                             66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _type="genomic DNA"
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                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                        Score 13.2; DB 10; Length 31; Pred. No. 1.1e+05; O; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fly)
                                                            GSS 06-MAR-2004
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                          Gaps
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              JOURNAL
PUBMED
REFERENCE
                                                                                                                                                                            REFERENCE
AUTHORS
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
AJ598495
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AUTHORS
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ORGANISM
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    AJ598495

AJ598495.1 GI:37948123
AJ598495.1 GI:37948123
GSS; right border; T-DNA flanking sequence.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Endaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Spermatophyta; Magnoliophyta; eudicotyledons; core Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana T-DNA flanking 469G03, genomic survey semicon
                                                                          T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002)
                                                                                                                                                               Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F. Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
2 (bases 1 to 33) Balzergue, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., P. Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., BAC end sequences of Library RP-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes
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                                                                                                                                                                                                                                                                                  osids; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCATATTTATGGAATG 19
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-072D07.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Pan troglodytes"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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83.3%;
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Pred. No. 1.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence, right
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                  Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 15-JAN-2004
border, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, Email: cdna@lgsun.grc.nia.nih.gov Plate: L0524 row: A column: 08 Sep primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Systematic Analyses of NIA Mouse Newborn Heart
Unpublished (2001)
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 вит23391 73 bp mRNA linear L0524A08-3 NIA Mouse Newborn Heart cDNA Library Mus clone L0524A08 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 73)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM123391.1 GI:17107159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piao, Y., Kargul, G.J., Dudekula, D.B., and Ko, M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATATTTATGGTATG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATATTTATGGAATG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF12907.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                   primer [Invitrogen: 5', particle with T4 DNA 24.9 microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal3 (Ref. Development 127:1737-1749 (2000) [PMID: 10725249]), purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were digested linkers by Centricon 100. Then, the cDNAs were digested
                                                                                                                                                                                                         /clone_lib="NIA Mouse Newborn Heart cDNA Library" /note="Organ: heart; Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2: Notl; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). Double-stranded cDNAs, were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Newborn Heart"
/dev_stage="Newborn"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:L0524A08-3."
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="L0524A08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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93.3%;
Sall and NotI enzymes, and cloned into Sall and NotI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No. 8.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qian, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pantano, S.,
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AUTHORS
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CL872413
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    ACCESSION
                                                                          DEFINITION
                                                                                                                                                RESULT 27
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                                                                                                                     CZ469014/c
                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 14
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JOURNAL
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CZ469014 31 bp DNA linear GSS 29-APR-2 C04137-Sprime Exelixis piggyBac PB insertions Drosophila melanogaster genomic Sequence recovered from 5' end of piggyBac, genomic survey sequence.

CZ469014
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                                                                                                                                                                                                                                                                                                                  Conservative
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FEATURES

POLYA=Yes

source

67.0%; 93.3%;

Score 13.4; DB Pred. No. 9.6e+C Mismatches

.6e+04; 10;

Indels Length

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Gaps

0

repaired and

GSS 29-APR-2005

0

COMMENT

TITLE JOURNAL AUTHORS

REFERENCE

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site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with ligation mixture by the chemical method. The average insert size is about 1.8 kb. The library was constructed by Yulan Piao (NIA)."
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CL872413 78 bp DNA linear GSS 30-AUG-20 abe80g07.x1 Soybean methylation filtered genomic library Glycine max genomic, genomic survey sequence.
CL872413 CL872413.1 GI:51603164
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Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max
                                                                                                                                                                                                                                                                                                                                  LibID: 227
Class: methylation filtered
                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 573-884-1267
Fax: 573-882-0588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylation filtered genomic sequences from Glycine max Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycine max (soybean)
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Similarity 93.3%;
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                                                                                                                                                                                                                                                                                                                                                           staceyg@missouri.edu
227
/tissue_type="Young leaves"
/clone_Tib="Soybean methylation filtered genomic library"
/clone_Tib="Soybean methylation filtered genomic library"
/note="Vector: pOT2; Site_1: BstXI; Randomly sheared
genomic DNA ranging from 0.7-1.5 kb were end repaired and
ligated to BstXI linkers prior to cloning in BstXI-cut
pOT2. LibID: 227"
                                                                                                                                                                                          /organism="Glycine max"
/mol_type="genomic DNA"
/cultivar="Williams 82"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                    db_xref="taxon:3847"
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Pred. No. 9.5e+04;
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RESULT 25 BM123391

VERSION ACCESSION DEFINITION

KEYWORDS

ORGANISM

Mus musculus

밁 ş

32 ហ ORIGIN

Query Match Best Local S Matches 14

Similarity

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ACCESSION
VERSION
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                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P. Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC884465 79 bp DNA linear GSS 31-JUL-2003 SALK 113190.28.40.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 113190.28.40.x, genomic
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                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                               Class: TDNA tagged
                                                                                                                                                                                                                  This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC884465.1 GI:33360821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAAATATTCATGGAATGA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCCATATTTATGGAATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 79)
                                                                                                                                                                                                                                                                          858 453 4100 x1752
858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.11, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                 ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
                         /mol_type="genomic
/ecotype="Col-0"
                                                                           organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UUGC1M0558007"
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/db_xref="taxon:10090"
xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.6; DB 9;
Pred. No. 7.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0555 row: P column: 09
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University of Utah
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AZ761406
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SALK_113190.28.40.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_musculus_C57BL/6J_(male)_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_obtained_from_the_Jackson_was_
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                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
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/clone="UUGC1M0555P09"
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/strain="C57BL/6J"
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Pred. No. 7.7e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              libraries, hybridizating of single-stranded DNA, semoving of remaining single-stranded DNA, digesting of regions comprising double-stranded DNA by a set of 4 bp-cutters, capturing of DNA hybrids with loop structures (alternative spliced exon), ligating of Y-shaped primers to isolated DNA hybrids with loop structures, PCR amplification of isolated DNA hybrids with loop structures, PCR amplification of ligation products and their cloning into pFLCI vector. (Reference)
                                                                                                                                                                                                                                                                                                                                                                                     survey sequence.
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Submitted (15-SEF-2004) Yoshihide Hayashizaki, The Institute
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Hori,F., Imotani,K., Kawai,J., Kondo,S., Murata,M., Nakamura,M.,
Nomura,K., Ohno,M., Sasaki,D., ShiraKi,T., Waki,K., Watahiki,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Libraries enriched for alternatively spliced exons reveal splicing patterns in melanocytes and melanomas Nat. Methods 1, 233-239 (2004)
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                                                                                                                                                                                  Maize genomic sequences 
Unpublished (2001)
                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 75)
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
                                                                                855 California Ave, Palo Alto, CA 94304,
Tel: 650 723 2227
                                                                                                                        Stanford University
                                                                                                                                         Department of Biological Sciences
                                                                                                                                                               Contact: Walbot
                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTCATCGTCATGGAATGA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCCATATTTATGGAATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 74)
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                                                             650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="mixture of B16-F10Y and melan-c" /cell_type="mixture of melanoma cell and melanocyte cell" /clone_lib="Alternative Splicing Library L2" /note="strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST00000035194, based on BLAT search"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="Y0G0128F23"
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.6; DB 4;
Pred. No. 7.6e+04;
                                                                                                                                                                                                       found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  u Grid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic,
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AZ763306/c
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ORGANISM
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Class:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Euarchontoglires; Glires;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 79)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1M0558007R Mouse 10kb plasmid
clone UUGC1M0558007 R, genomic
                                                                                                                      Insert Length: 10000 Std Error: Plate: 0558 row: O column: 07 Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0558 row: O column: 0
                                                                                                                                                                                                                                                                  University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ763306.1 GI:12874201 GSS.
                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                                                                                  High quality sequence stop:
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                                                                                                          ass: plasmid ends
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transposon-tagge
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  organism="Mus musculus"
/mol_type="genomic DNA"
                                                             Location/Qualifiers
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/clone lib="1119 - RescueMu Grid AA"
/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DNA"
cultivar="mixed background W23/A188/B73/K55"
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Score 13.6; DB 10 Pred. No. 7.6e+04; DB 10; Length Indels 75; 0, Gaps 0

genomic survey sequence bp DNA linear GSS 16-FEB-20
UUGC1M library Mus musculus genomic GSS 16-FEB-2001

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia;

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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2030 E.,

SLC, 딝

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REFERENCE
AUTHORS
TITLE
                                    ORIGIN
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CD998266/c
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QBF11a10.xg (
CD998266
CD998266.1 (
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                                                                                                                                                                                                plant genomics programme 'Genoplante' (ht
and http://genoplante-info.infobiogen.fr)
                                                                                                                                                                                                            This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                Genoplante
                                                                                                                                                                                                                                                                                                                                Genoplante, a major partnership french program in plant Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                   Genoplante.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At1g79580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCACACATTTAATGAATGA 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="SALK 143526.52.25.n"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                /tissue_type="ear leaf"
/clone_lib="QBF"
                                                                                                               organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
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                                                                              clone="QBF11a10"
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                                                                                                                                                                                location/Qualifiers
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/mol_type="genomic DNA"
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/db_xref="taxon:3702"
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 Score 13.6;
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Pred. No. 7.5e+04;
0; Mismatches 4
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A clone QBF11a10, mRNA
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AK184042
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Best Local Similarity
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Mus musculus
Mus musculus
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                                                                                                                                                                                                                                    Mus musculus cDNA, clone:Y0G0128F23, strand:minus, reference:ENSEMBL:Mouse-Transcript-ENST:ENSMUST00000035194, based on BLAT search.
                  Watahiki,A.,
Nakamura,M.,
                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                               AK184042
AK184042.1 GI:56008219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Martienssen RA
Cold Spring Harbor Laboratory
Bungtown Rd., Cold Spring Harbor,
                                                                                                                                                                                                                                                                                                  AK184042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX199598 73 bp DNA linear GSS 03-JAN-2 AY199598 Arabidopsis thaliana Landsberg DNA Arabidopsis thaliana genomic clone ET6618.Ds5.12.01.99.b.73, genomic survey sequence. AY199598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: martiens@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 516 367 8322
Fax: 516 367 8369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis genomic sequences flanking in transgenic lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyrosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                 TCTCGATATTTTTGGTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/cultivar="ecotype Landsberg"
/db xref="taxon:3702"
/clone="ET6618.Ds5.12.01.99.b.73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to 73)
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Waki,K., Hayatsu,N., Shiraki,T., Sasaki,D., Arakawa,T., Kawai,J., Y. and Carninci,P.
                                                                                                                                                          (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.0%;
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Pred. No. 7.
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0; Mismatches 4
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                  Kondo,S.,
Harbers,M.,
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                                                                                                                   Euteleostomi;
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                                                                                                                                                                                                                                                                                                HTC 23-NOV-2004
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RESULT 16
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AUTHORS
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AA152920/c
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 64)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
Waterston, R.
The Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurgnathi; Muridea; Muridae; Murinae; Mus.
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AA152920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA152920 64 bp mRNA linear EST 11-FEB-1997 mmr89f02.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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BI558013
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                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                         /dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ; heart; Vector; pBluescript SK; Site_1:
RcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:604635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="pooled"
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Pred. No. 7.5e+04;
0; Mismatches 4
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Pred. No. 7.4e+04;
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 TIRNA
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linear
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 EST 05-SEP-2001
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AUTHORS
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       TITLE
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1 (bases 1 to 65)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., P.
Shinn,P., Simmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 65)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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BI558013
BI558013.1 GI:15445327
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Location/Qualifiers
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                                                                                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                           BZ770591
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                                                                                                                                                                                                                                                                   BZ770591.1 GI:28944275
                                                                                                                                                                                                                                                                                                               survey sequence.
                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                        rosids; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCCATATTTATAAAGTTA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCCATATTTATGGAATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Notl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DHIOB"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:5293540"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%;
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Pred. No. 7.5e+04;
0; Mismatches 4;
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                                                                                                                           Arabidopsis.
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                                                        Prednis, L.,
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RESULT 13
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LOCUS
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AUTHORS
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ORGANISM
ORIGIN
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH790339 31 bp DNA linear GSS SALK 056850.37.80.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK 056850.37.80.x,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                      Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker
Salk Institute Genomic Biological Studies
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Genome 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS
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Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCATATTTATGGAAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 31)
                                                                                                                                                                                                                                                                                                                                                                                                    is single pass sequence recovered from
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858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                             ecker@salk.edu
              directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                     /clone="SALK_056850.37.80.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clome_lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                       /mol_type="genomic
                                                                                                                                                                                                                                                                                organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                              db_xref="taxon:3702"
                                                                                                                                                                                                                                    ecotype="Col-0"
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|mol_type="mRNA"
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lone="TEgg038f23"
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.8; DB 5;
Pred. No. 6.1e+04;
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JOURNAL COMMENT
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AUTHORS
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VERSION
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CB275155
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. This is a Oligo (dT)-SL1 PCR based library. cDMA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo (dT) on the 3' end were non-directionally cloned into pCRII-TOPO (Invitrogen) following the TOPO TA cloning protocol. Parasitic adult females were collected from immunologically naive animals and provided by Dr. Mark Viney (Mark Viney@bristol.ac.uk) of University of Bristol, Bristol, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: McCarter JP
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative full length read The vector to vector length is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Washington Univ. Nematode EST Project, 1999 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptce, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Panagrolaimoidea; Strongyloididae; Strongyloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongyloides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ku58h05.y1 Strongyloides ratti PA female na Strongyloides ratti cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: SL1 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongyloides ratti
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                est@watson.wustl.edu
                      Site 2: ECORI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. This is a Oligo(dT)-SL1 PCR based library. cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Parasitic adult females were collected from immunologically naive animals and provided by Dr. Mark Viney (Mark Viney@bristol.ac.uk)
of University of Bristol, Bristol, UK.
                                                                                                                                                                                                                                                                                                                                                    /dev_stage="Parasitic adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                      note="Vector:
                                                                                                                                                                                                                                                                                                                        clone_lib="Strongyloides ratti PA female naive SL1 TOPO
                                                                                                                                                                                                                                                                                                                                                                                                           /sex≃"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:34506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Strongyloides ratti"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                        pCRII-TOPO (Invitrogen); Site_1: EcoRI; The library was constructed by Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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CN924729
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1 TCCCCATATTTATGGAA 17
||||| ||| |||| ||||
12 TCCCCAGATTTACGGAA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B
McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E.
HortResearch Apple EST Project
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
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CN924729.1 GI:48397542
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN924729 73 bp mRNA line 000415AELA008286HT (AELA) Royal Gala young expa domestica cDNA clone AELA008286, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malus x domestica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Gleave, A.
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                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                     /organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
                                                                                                                                                                                         /dev_stage="Young, expanding"
/clone_lib="(AELA) Royal Gala young expanding
/note="Vector: pBK-CMV; Library sequenced by G
Research & Development"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                           tissue_type="Leaf"
                                                                                                                                                                                                                                                                                                      clone="AELA008286"
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88.2%;
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Pred. No. 6.1e+04;
                                                                                                        Score 13.8; DB 7;
Pred. No. 6.1e+04;
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HMGS00884 Human promyelocyte Homo sapiens cDNA clone mm2371
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BX783453
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA sequencing
Unpublished (1993)
Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T.,
Yoshinari,H., Arimoto,J. and Matsubara,K.
Institute for Molecular and Cellular Biology
Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y., Yoshinari, H., Arimoto, J. and Matsubara, K. Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from
ECORI-NotI cut cDNA was then ligated into pCS107 with
                                                                               Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TEgg038f23.qlkT7
Sequencing primer: T7
                                                                                                                                                                                                        Sanger Xenopus tropicalis 
Unpublished (2003)
                                                                                                                                                                                                                  1 (bases 1 to 79)
1 (bases 1 to 79)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. a
                                                                                                                                                                                                                                                                                                                                      Xenopus tropicalis (western clawed frog) Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                               BX783453.1
EST.
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                                                      Sequencing primer: T7
This sequence is from a Xenopus Gene Collection (XGC) library
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 88.2
15; Conservative
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                                                                                                                                                                     Sanger Institute
                                                                                                                                                                                          Contact: Croning MDR
                                                                                                                                                                                                                                                                                  (enopodinae; Xenopus; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line =
promyelocyte. "
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/db_xref="taxon:9606"
/clone="mm2371"
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88.2%;
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Pred. No. 6.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro.
Plate: 0318 row: J column: 16
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1M0318J16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0318J16 F, genomic survey semuence
AZ48816F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 59)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 59.
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/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.isetate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                                 musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
was hydrodynamically sheared by repeated passage through
                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DH10B cells were transformed and then screened on LB plates with ampicillin."
                       (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                  mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                 'sex="Male"
                                                                                                                                                                                                        clone="UUGC1M0318J16"
                                                                                                                                                                                                                                   db_xref="taxon:10090"
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88.2%;
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Pred. No. 5.9e+04;
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AZ471628/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. W.
University of Utah G.
University of Utah
Rm. 308, Biomedical I
                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0286 row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                               Seq primer: CGTTGTAAAACGACGGCCAGTClass: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 72)
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GSS.
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                                                                                                                                                                                                                                                                                                                        quality sequence stop: 72.
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801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/5"
/db xref="taxon:10090"
/clone="UUGC1M0286B20"
musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
                                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                             'sex="Male"
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88.2%;
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Pred. No. 6e+04;
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                    from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA

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                                                                                                                                                                                                                                                                                                                                                                                                            Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR403306 51 bp I
Arabidopsis thaliana T-DNA flanking
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence
                                                                                                                                                                                                                          An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR403306.1 GI:46944034
                                                                                              High-throughput generation of sequence indexes from mutagenized Arabidopsis thaliana lines
                                                                                                                                         Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
                                                                                                                                                                                                                                                                                                              Rosso, M.G.,
                                                                                                                                                                                                                                                                                                                                                                        Bioinformatics 19 (11), 1441-1442 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
  Direct Submission
                       Strizhov, N.,
                                                                               BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                           Weisshaar,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                      (bases 1 to 51)
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/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
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/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon: 4577"
/tissue_type="leaf"
/dev_stage="adult"
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                     R0880, M.G.,
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Pred. No. 5.9e+04;
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                     Li,Y. and Weisshaar,B
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CG720219
CG720219.1 GI:3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                Reverse complemented post-ligation sequence plate: 1119061 row: 26 Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 650 723 2227
Fax: 650 725 8221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize genomic sequences found using engineered RescueMu transposon
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Similarity 88.2%;
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/db_xref="taxon:3702"
/clone="GX-862C12-025976"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                    /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
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Pred. No. 5.9e+04;
0; Mismatches 2;
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                                                   BZ381604 33 bp DNA linear GSS 26-NOV-2002 SALK 116995.26.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_116995.26.55.x, genomic
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                    BZ381604
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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48 bp DNA linear GSS 02-APR-2002 SALK 063412.45.95.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 063412.45.95.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker
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                                                                                                                                                                                                                                                                                                                                                                        /clone="SALK_063412.45.95.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
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80.0%;
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Pred. No. 3.6e+04;
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                                     Stanford University
855 California Ave, Fel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 CATATTTATGGAAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 33)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Email: walbot@stanford.edu
Very probable ligation sito
                                                                                                                                          Unpublished (2001 Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                        survey sequence.
CG720973
CG720973.1 GI:37754383
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                     Department of Biological
                                                                                                                                                                                                    Walbot, V.
                                                                                                                                                                                                                                                                                                     Zea mays
                                                                                                                                                                                                                                                                                                                         Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                          1119064G08.1EL_x1 1119 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; rosids; eurosids II; Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                 Maize genomic sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATATTTATGGAAT
                                                                                                                                                                                                                        (bases 1 to 51)
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858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="SALK_116995.26.55.x"
/clone lib="Arabidopsis thallana TDNA insertion lines"
/clone lib="Arabidopsis thallana TDNA insertion lines for the process of the lines one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
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                                                                              Palo Alto, CA 94304, USA
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    gite
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                                                                                                                       Sciences
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RescueMu
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    of ends
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  cut by single endonuclease.
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AI099326/c
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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12.4
12.4
12.4
12.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra, M., Hillier, L., Allen, M., Bowles, M., Districh, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI099326.1 GI:3448851
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:930875
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                       igated to a Draili adaptor [TGTTGGCCTACTGG], digested and cloned into distinct Draili sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). Xhol should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                /clone_lib="Sugano mouse liver mlia"
/note="Organ: liver; Vector: pMELBS-F13; Site_1: DraIII
/CACTGTGTG]; Site_2: DraIII (CACCATGTG); 1st Strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                      dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                     'sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="taxon:10090"
'clone="IMAGE:1482519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="mRNA"
|strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                        lab_host="DH10B"
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BQ541987 ps91f02.y
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AZ776733 ZM0010E07
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Query Match

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Score 15.8;

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Length

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University of Utah Ge
University of Utah
Rm. 308, Biomedical F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
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1M0241G06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0241G06 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: (
Plate: 0241 row: G column: 06
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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801 585 7177
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Location/Qualifiers
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the Dlunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC1M0241G06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                     Key
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Antisense compounds targeted to nucleic acid encoding telomeric repeat binding factor 2 useful for treating conditions such as premature agin
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel antisense compound (I) 8-30 nucleobases in length targeted to a polynucleotide encoding human telomeric repeat binding factor 2 (II) which specifically hybridizes with, and inhibits the expression of (II). (I) is useful for treating a human having a disease or condition associated with (II) such as premature aging or a hyperproliferative disorder especially cancer, by inhibiting the expression of (II) in human cells or tissues. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. The products of the invention have cytostatic activity. This sequence represents an antisense oligonucleotide used to illustrate the method of the invention.
                                                                                                                                                                                                                                 04-JUN-1999;
25-MAY-2000;
09-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                     Airway hyperresponsiveness; pulmonary antisense oligonucleotide; human; B7 antiasthmatic; antiinflammatory; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human B7-2 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and diseases such as cancer.
                                                                                      Treating airway hyperresponsiveness or pulmonary inflammation comprises administering an antisense compound targeted to a nucleic acid molecule encoding a human B7 protein to the individual.
                                                                                                                                                                                  (BENN/)
(VICK/)
(KARR/)
                                                                                                                                                                                                                                                                   31-DEC-1996;
                                                                                                                                                                                                                                                                                          23-MAY-2003;
                                                                                                                                                                                                                                                                                                                 05-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ54571 standard; DNA;
                                                                                                                                                            Bennett CF,
                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                       2004-132608/13.
                                                                                                                                                                                                                                                                                                                                                              sapiens.
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                                                                                                                                                                                  KARRAS J G.
                                                                                                                                                                                             BENNETT C F.
VICKERS T A.
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; 99US-00326186.
; 2000WO-US014471.
; 2001US-00851871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                              Vickers
                                                                                                                                                                                                                                                                                           2003US-00444206
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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8
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                protein; B7-2;
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The invention relates to a method for trea or pulmonary inflammation in an individual antisense compound targeted to a nucleic a B7 protein. The invention also relates to

to a method for treating airway hyperresponsive ion in an individual comprising administering

hyperresponsiveness

þ human

acid molecule encoding a method of inhibiting coding B7-1 or B7-2. The

Example 27;

SEQ ID

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391; 182pp; English.

expression of

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RESULT 27
AA178771/c
ID AA1787
XX AA1787
XX Human
XX Human;
KW Protei
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YX Human;
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AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide sequences (1), which contain single nucleotide polymorphisms (SNPs). AAM53114 to AAM53329 represent peptides related to human polymorphic polymucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or deletions in a patient's genome that affect the activity of polypeptides
                                                                                                                                                                                                                                                                                             Claim 1; Page 2258;
                                                                                                                                                                                                                                                                                                                                                                                  Polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets
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29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quantitation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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14; Conser
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93.3%;
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Pred. No. 9
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RESULT 28
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Best Local S
Matches 14
The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 5912 nucleotide sequences, appearing as ABX50072-ABX55983, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non- translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any
                                                                                                                                                                              Claim
                                                                                                                                                                                                     Purified nucleic acid molecules, useful for genome mapping, identification and analysis, cattle breeding or preparation for cattle gene expression and genetically improved cattle.
                                                                                                                                                                                                                                                                  WPI; 2003-102386/09
                                                                                                                                                                                                                                                                                               Byatt
                                                                                                                                                                                                                                                                                                                                        (BYAT/) |
(MATH/) |
(TAON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polymentides.
                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998;
15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-2001;
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                                                                                                                                                                                                                                                                                               JC,
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                                                                                                                                                                                                                                                                                                                                                                                              98US-0113678P
99US-00465231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fat deposition; genome mapping;
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breeding
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Pred. No. 9.7e+03
                                                                                                                                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lactation; LMFD;
                                                                                                                                                                                                                                                                                               WC;
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The invention relates to short interfering nucleic acids (siNA) which CC downregulate expression of the human transforming growth factor beta CC (TGFb) receptor (TGFb-R) gene by RNA interference. The siNAs may or may CC not comprise ribonucleotides and may be double or single stranded. They CC further comprise sense and antisense regions, or alternatively are CC assembled from a sense oligonucleotide and an entisense oligonucleotide. Specifically, the siNAs include short interferening RNA (siRNA), double-CC stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs CC can be unmodified or chemically modified, can contain CC deoxyribonucleotides, and can be chemically synthesised, expressed from a CC vector or enzymatically synthesised. The invention also relates to kits Cfor the in vitro or in vivo delivery of siNA, conjugates and/or complexes CC expression of the TGFb-R gene in cells, tissue explants or organisms CC (e.g., by ex vivo gene therapy), or in grafts and transplants for the treatment of a variety of conditions. They may be used for treating CC diabetic nephropathy, chronic liver disease or pulmonary fibrosis. The siNAs are also useful for drug screening, diagnosis, therapeutic target CC studying gene function, and gene mapping (e.g., of single nucleotide CC polymorphisms). The present sequence represents the lower strand of a CC human TGFb-R-targeted double-stranded siNA.
                                                                                                                        Query Match
Best Local S
Matches
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11-MAR-2002;
06-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmacogenomics; gene function analysis; gene mapping; human; antidiabetic; nephrotropic; hepatotropic; cytostatic; transforming growth factor beta receptor; TGFb; TGFb-R; diabetic nephropathy; chronic liver disease; pulmonary fibrosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New short interfering nucleic acid, useful e.g. for treatment and diagnosis of diabetic nephropathy, which downregulates expression transforming growth factor-beta receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA; expression modulation; gene therapy; drug screening; diagnosis; therapeutic target identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-697557/66.
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05-SEP-2002;
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                                                                                                                                                                                                                                                   Sequence 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-2002;
                                                               σ
                                                                                                                                                         Similarity
AUAUUUAUGGAAUCA 15
                                                               ATATTTATGGAATGA
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                                                                                                                                                                                                                                                   BP; 7 A; 2 C; 3 G; 0 T; 7 U; 0 Other
                                                                                                                              Conservative
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2002US-0425559P.
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2002US-0408378P.
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2002US-0386782P.
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                                                                                                                                                  67.0%;
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                                                                                                                                                            Pred.
                                                                                                                                                                                          Score 13.4;
                                                                                                                              Mismatches
                                                                                                                                                      9e+03;
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                                                                                                                                                                                          DB 10;
                                                                                                                              Indels
                                                                                                                                                                                    Length
                                                                                                                                                                                              19;
                                                                                                                              0
                                                                                                                              Gaps
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RESULT 26

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CC family kinase inhibitor for treating asthma. Where the asthma is statima, at-risk haplotype in MAPSK9 gene, polymorphism in MAPSK9 nucleic cc acid, dysregulation of MAPSK9 mANA expression, dysregulation of a MAPSK9 comman at-risk haplotype for cc acid, dysregulation of MAPSK9 mANA expression. The invention cc further comprises: a method for the diagnosis or identification of conclusions of diagnosing asthma, a method for the use of a first nucleic acid conclusions for diagnosing asthma or susceptibility to asthma in a sample; a cc method for assaying the presence of a first nucleic acid molecule in a cc method for assaying the presence of a first nucleic acid molecule; a method for assessing the response to treatment with an MLK cc family kinase nucleic acid inhibitor in a target population or in an cc individual with an at-risk haplotype for asthma, at-risk haplotype in the MAPSK9 mana, at-risk haplotype in the MAPSK9 mana, at-risk haplotype in the mapsky gene, polymorphism in the MAPSK9 nucleic acid, dysregulation of MLK1 protein isoform expression, increased MLK1 biochemical activity or increased Cc MLK1 protein isoform expression; a method for assessing the response to treatment with an at-risk haplotype for asthma, as above; a kit for assaying a sample for the presence or astence or astence or at least one haplotype comprising 2 or more alleles associated with asthma comprising; at least one haplotype, and reagent kit for assaying the presence of at least one haplotype in the presence of at least one haplotype at least one haplotype. The for the presence of at least one specific allele of comprising at least one nucleic acid capable of detecting the presence of at least one haplotype and a reagent kit for assaying at least one haplotype. The presence of at least one haplotype and a reagent kit for assaying at least one haplotype. The presence of at least one haplotype and a reagent kit for assaying at least one haplotype and a reagent kit for assaying at least one haplotype. The must form the presence o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of mixed lineage kinase family kinase inhibitor in the manufacture a medicament for treatment of asthma associated at-risk haplotype for asthma, at-risk haplotype in MAP3K9 gene or increased MLKI protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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05-APR-2004; 2004US-0559611P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP3K9 marker amplification forward primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hakonarson H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to the novel use of a mixed lineage kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENETICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; antirheumatic;
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RESULT 24
ADJ66231/c
ID ADJ662
XX ADJ662
XX O6-MAY
DT O6-MAY
XX Human
XX RNA in
KW RNA in
KW Short
KW Shorn
KW 
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Best Loc
Matches
                                                                                                         RNA interference; short interfering nucleic acid; siNA; short interfering RNA; siRNA; double-stranded RNA; micro-RNA; miRNA; short hairpin RNA; shRNA; expression modulation; gene therapy; drug screening; diagnosis; therapeutic target identification; pharmacogenomics; gene function analysis; gene mapping; human; antidiabetic; nephorotropic; heparotropic; cytostatic; transforming growth factor beta receptor; TGFb; TGFb-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcriptome comprises messenger RNAs transcriptome, where the (sub-
transcriptome comprises messenger RNAs transcriptom multiple
transcription units that populate a genome. The library comprises several
oligonucleotides, each capable of hybridising selectively to a set of
messenger RNAs transcribed from a given transcription unit of the genome,
which encodes one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from a
biological sample, in expression profiling studies.
                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ66231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADJ66231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present inv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shoshan
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                                                                                                                                                                                                                                                                                                                                    TGFb-R
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                                                                                  nephropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; RNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCCATATTTATGGAATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes oligonucleotide libraries AB that populate a (sub-)transcriptome, where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wasserman
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                                                                                                                                                                                                                                                                                                                                 transcript target sequence/siNA upper strand,
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2001US-0287724P.
                                                                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.0%;
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                                                                                     chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۶,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 G; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 13.6; DB 6;
Pred. No. 7.8e+03;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                  disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                  pulmonary fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                 SEQ
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Homo sapiens

Human TGFb-R siNA lower strand,

SEQ

ID NO:197

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Gaps

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RESULT 25
ADJ66359
ID ADJ66
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AC ADJ66
DT 06-M2
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DB Humar
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Matches
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                                                                                                                                                                                                                                                                                                                                deoxyribonuclectides, and can be chemically synthesised, expressed from a vector or enzymatically synthesised. The invention also relates to kits for the in vitro or in vivo delivery of siNA; conjugates and/or complexes of siNA; and vectors that express siNA. The siNAs are used to modulate expression of the TGFb-R gene in cells, tissue explants or organisms (e.g., by ex vivo gene therapy), or in grafts and transplants for the treatment of a variety of conditions. They may be used for treating diabetic nephropathy, chronic liver disease or pulmonary fibrosis. The siNAs are also useful for drug screening, diagnosis, therapeutic target identification and validation, genetic engineering, pharmacogenomics, studying gene function, and gene mapping (e.g., of single nucleotide polymorphisms). The present sequence represents the upper strand of a human TGFb-R-trargeted double-stranded siNA, which is identical to the TGFb-R trargeted double-stranded siNA, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAR-2002;
06-JUN-2002;
06-JUN-2002;
29-AUG-2002;
05-SEP-2002;
09-SEP-2002;
                                            06-MAY-2004
                                                                        ADJ66359;
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further comprise sense and antisense regions, or alternatively are assembled from a sense oligonucleotide and an ense oligonucleotide. Specifically, the siNAs include short interfering RNA (siRNA), double-stranded RNA, micro-RNA (miRNA) and short hairpin RNA (shRNA). The siNAs can be unmodified or chemically modified, can contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New short interfering nucleic acid, useful diagnosis of diabetic nephropathy, which transforming growth factor-beta receptor
                                                                                                    ADJ66359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    downregulate expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention
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15-JAN-2003;
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                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to short interfering nucleic acids (siNA) which invention regulate expression of the human transforming growth factor betains receptor (TGFb) gene by RNA interference. The siNAs may or comprise ribonucle
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                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                         transcript
                                                                                                                                                                                                                                                 Similarity
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                                                                                                    standard; RNA; 19
                                                                                                                                                                           ATATTTATGGAATCA
                                                                                                                                                                                                       ATATTTATGGAATGA
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                                                                                                                                                                                                                                                                                            BP;
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; 2002US-0408378P.
; 2002US-0409293P.
; 2002US-0425559P.
; 2003US-0440129P.
                                                                                                                                                                                                                                     Conservative
                                          (first entry)
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2002US-0386782P.
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                                                                                                                                                                                                                                                                                                                         target sequence.
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93.3%;
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Pred. No. 9e
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                                                                                                                                                                                                                                                               DB 10;
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SiNAs

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RESULT 22
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                            present invention describes these oligos as useful for uncleic acids and in particular for profiling mRNA splice variants, detecting mutations, deletions or duplications that may be associated with onset or increased risk of diseases such as cancer. Accordingly, such oligos exhibit cytostatic activities. Furthermore, these LNA such oligos exhibit cytostatic activities. Furthermore, these LNA such oligos exhibit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to novel non-naturally occurring nucleic acids that exhibit enhanced biostability and capture efficiency i.e. hybridisation. Specifically, it refers to locked nucleic acid (LNA) oligos that have restricted flexibility in the ribofuranose ring of the nucleoside due to the presence of a 2'-O, 4'-C methylene bridge. The present invention describes these oligos as useful for detecting target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                          containing oligos can be used as fluorescent in situ hybridisation (FISH) probes or on diagnostic microarrays to detect splice isoform signatures, as well as antisense oligos that can modulate or silence sense nucleic acid agents. This oligonuclectide sequence is a DNA oligo capture probe (that can optionally be LNA-modified) given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-naturally-occurring nucleic acid having a melting temperature and capture efficiency higher than a control nucleic acid, useful for detecting and amplifying target nucleic acid, for alternative mRNA splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kauppinen S,
Arctander P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EXIQ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-OCT-2002;
19-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-2003;
                                                                                                                                                                                                                                                                                                                   Sequence 50
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ss; expressed sequence tag;
                             Eucalyptus
                                                           16-DEC-2004
                                                                                         ADS53601;
                                                                                                                   ADS53601 standard;
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                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                           TCCCCATATTTATGGAATGA 20
                                                                                                                                                                                               TTCACATATTTATCGATTGA
                             wood forming tissue expressed sequence tag #1155
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                   BP; 18 A; 11 C;
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2003DK-00000752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alsbo C,
Tommerup
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "OTHER= Optionally a locked nucleic acid (LNA) exists at every third position (LNA-3). All LNA cytosines are methyl cytosines."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _mod_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note = "OTHER= Optionally this is a locked nucleic acid (LNA). All LNA cytosines are methyl cytosines."
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                                                                                                                   DNA;
                                                                                                                                                                                                                                                                       68.0%;
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EST;
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                                                                                                                                                                                                                                                                                                                   11 G; 10 T; 0
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                                                                                                                                                                                                                                                                                   Score
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                                                                                                                                                                                                                                                          Mismatches
gene
                                                                                                                                                                                                                                                         a 13.6; v.
vo. 7.7e+03;
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expression;
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                                                                                                                                                                                                                                                                                     DB 13; Length 50;
                                                                                                                                                                                                                                                                                                                   U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a DNA (I) that shows increased or decreased cc expression during biosynthesis of cell wall components or formation of cc wood fibre cells in a plant, comprising a nucleotide sequence that chybridises under stringent conditions with any of 1731 fully defined cc sequences (S1) of 60 nucleotides given in specification, or with a cnucleotide sequence encoding a protein having 50% or more homology with ct that encoded by (S1). Also included in the specification are: (a) a cc promoter DNA (II) of (I); (b) a DNA comprising a nucleotide sequence that cc is complementary to (I) or nucleotide sequence that codes RNA, which cc suppression effect; (c) a recombinant vector (III) comprising (I); (d) a comprising (III); and (f) a transformed plant cell (IV) cc comprising (III); and (f) a transformed portion (V) obtained from (CC incorphological formation of wood fibre cells. This sequence corresponds to an expressed sequence tag (BST) fragment relating to the DNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes specifically expressed in eucalyptus wood forming tissues, useful in controlling biosynthesis of cell wall components and morphological formation of wood fiber cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hibino T;
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                                                                                                                                                                                                                                                                                                                            Mouse spliced transcript detection oligonucleotide SEQ ID NO:26954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-677544/66.
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   20-JUL-2001; 2001WO-IB001903.
                                                              07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN54206;
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                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN54206 standard; DNA; 65
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                                                                                                                                                                                                                                            variant; transcriptome; oligonucleotide
                                                                                                                                                                                                                                                                    mouse; rat; splice transcript; detection; RNA transcript;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCCCTTATATATGTTATGA 41
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВÞ
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Pred. No. 7.8
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RIKEN

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AAZ66376
ID AAZ66376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC one polymorphisms may be identified in a nucleic acid sample using probes or compolymorphisms may be identified in a nucleic acid sample using probes or comprisers specific for a sequence selected from ABZ43217-ABZ50887 using a compriser specific for a sequence selected from ABZ43217-ABZ50887 using a compression of the compression assays, nucleic acid compression and probable of compression and probable of compression and probable of compression and screening drugs using genetic polymorphism data, particularly that relating to single nucleotide complymorphism data, particularly that relating to single nucleotide complymorphisms (SNPs), may be used in studying the relationship between complymorphism data, particularly that relating to single nucleotide complymorphism data, genetic polymorphism data, genetic complymorphism data, conditions, and responses to complymorphism are also useful as polymorphism data, conditions, occur complymorphism genetic complymorphism complymorphisms. SNPs are particularly useful complymorphism strip are stable of individual particular particular particular particular particular particular particular partient, but would also comply take the guesswork out of selecting the drug with the complymorphism would not only take the guesswork out of selecting the drug with the complymorphism should also of the invention are also useful in the drug discovery and composition of the invention are also useful in the drug discovery and composition of the particular genetic profiles indicate that they are collineal trials only if their genetic profiles indicate that they are collineal trials only if their genetic profiles indicate that they are comply dependent of the invention may therefore lead to a an increase in the range of complymorphism data and compositions of the inventions, the time take
                Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; diagnosis;
                                                                                                                                            10-SEP-2001
                                                                                                                                                                                                                         AAZ66376 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences ABZ43217-ABZ50887 represent polymorphic sites within general encoding enzymes associated with drug metabolism. The invention relitomethods and compositions for identifying individuals who have at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying individuals having a polymorphism, useful for determining effectiveness or side effect of a drug or treatment protocol, comprise detecting at least one polymorphism in the drug metabolizing enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences ABZ43217-ABZ50887
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                                                                                                    map-related
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                          (first entry)
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                                                                                                    biallelic
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80.0%;
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Pred. No. 7.6e+03;
D; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                             Query Match
       Key
modified_base
                                                                                                                               02-DEC-2004
                                             Unidentified
                                                                                 biostability;
                                                                                                                                                                             ADS92006
                                                                                                     DNA oligo capture probe gene78.m0103
                                                                                                                                                                                                                                                                                                                                      Sequence 47
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23-NOV-1998;
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                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                        TCCCCATATTTAACGATTTA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blumenfeld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human genome.
                                                                                                                                                                                                                                                                                                                                     BP; 14
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                              (first entry
                                                                               cancer; cytostatic; diagnostic microarray; ss; probe;
                                                                     acid;
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                     Location/Qualifiers
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                     A; 9
                                                                                                                                                                              DNA;
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                                                                                                                                                                                                                                                                                               68.0%;
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                                                                                                                                                                                                                                                                                                            Score 13.6;
                                                                                                                                                                                                                                                                                                  Pred.
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                                                                                                                                                                                                                                                                                                  .6e+03;
                                                                                                                                                                                                                                                                                                             DB 3;
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                                                                                                                                                                                                                                                                                                            Length 47;
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RESULT 18
ABX67784/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single-stranded DNA for identifying gene signatures directed human cDNA library that reflects relative amRNA in specific human tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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  Helicobacter pylori
                                                                                                                              Novel Helicobacter
                                                                                                                                                                               07-MAY-2003
                                                                                                                                                                                                                                                                             ABX67784 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in a cDNA library can be determined (esp. using primers derived from the GS sequences) as a means of diagnosing
                                                      Protein-protein interaction; PCR; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCATATTTATGGAATG 19
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88.2%;
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Pred. No. 6.3e+03;
                                                                           ulcer; selected interacting
                                                                                                                              PCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 T; 0 U; 1 Other;
                                                                                                                              primer #755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 78;
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abnormal c
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
27-DEC-2000;
02-MAY-2001;
27-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This sequence represents a primer used to isolate polymucleotides encoding Helicobacter pylori proteins for studies on protein-protein interactions
                                                                                                                                                                                             Human; drug metabolising enzyme; gene; drug metabolism; polymorphic drug evaluation; drug screening; genotyping; genetic profiling; therapeutic customisation; adverse reaction; clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                               26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ulcers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventing
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                                                                   04-JUL-2002.
                                                                                                                                       Key
variation
                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                        Human carboxyl ester lipase CEL gene polymorphic site,
                                                                                                                                                                                                                                                                                                      ABZ50651;
                                                                                                                                                                                                                                                                                                                               ABZ50651 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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                                            27-DEC-2001;
                                                                                           WO200252044-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 BP; 14 A; 5 C; 3 G; 5 T; 3 U; 0 Other;
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2000JP-00399443.
2001JP-00135256.
2001JP-00256862.
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                                            2001WO-JP011592
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                                                                                                                                                 Location/Qualifiers
                                                                                                                                      replace (21,C)
                                                                                                            /*tag= a
/standard_name=
                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%;
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                                                                                                                  "Single nucleotide polymorphism
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No. 7.4e+03;
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17

CCAACATTTATGGAATG 1 CCCATATTTATGGAATG 19

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RESULT 15
AAAD04818/c
ID AAD048
XX AAD048
XX AAD048
XX Human
DT 17-JUL
XX Human
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XX Human
XX Homo s
PN W02001
XX PPN W02001
XX 23-OCT
XX 2
RESULT 16
ACI04232/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present DNA sequence is human leptin receptor gene exon 6 forward CC (13F) RT (Reverse Transcriptase)-PCR primer. This primer is used for amplifying human leptin receptor gene by RT-PCR from human abdominal fat mENA, which is used for screening an adipose tissue-derived chicken cDNA (11 corresponding DNA molecule. Leptin receptor is used for regulating corresponding DNA molecule. Leptin receptor is used for regulating corresponding bnA molecule. Leptin receptor is used for regulating consumption, fat deposition, puberty, thermoregulation, immunity, and energy expenditure. Leptin receptor is specifically used consumption, fat deposition, puberty, thermoregulation, immunity, and energy expenditure. Leptin receptor is specifically used for attenuating leptin activity in vivo (particularly using a soluble for attenuating leptin activity in vivo (particularly using a soluble form a transgene). Leptin receptor provides a replacement for the forced molting procedure to improve performance and profitablity of old laying hens. The invention correction is also used to isolate leptin gene and to establish a bioassay for leptin activity, e.g. to screen for birds with high or low leptin levels in the blood (e.g. for breeding purposes) and/or for isolation of
                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 21; 67pp; English.
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                                                                                                                        CCATATTTATGGGCTGA
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                                                                                                                                                                                                                                                                                                                                                                  7 A;
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                                                                                                                                                                                                                                                                   Score 13.8; DB 4;
Pred. No. 5.8e+03;
                                                                                                                                                                                                                                                                                                                                                              6 T; 0 U;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                  0 Other;
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AAT19807 ID AAT1 XX

AAT19807

standard;

CDNA

to mRNA;

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RESULT 17

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                                                                                                                  CC perfect match, perfect mismatch, antisense match or antisense mismatch.

CR Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, is compounds. The nucleic acid probes are specifically designed for analysis of genetic variation or in hybridisation of taglabelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises comparises the following at least one or more nucleic acids to at least two or more concluding at least one or more nucleic acids to at least two or more concluded analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, confidence acids further comprises a tag sequence. The array of nucleic acid concluded acids further comprises a tag sequence. The array of nucleic acid composes is useful in in situ hybridisation, in Southern, Northern or dottolled hybridisation to identify or detect the sequence or specific contactions of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening CDNA or genomic libraries or subclones
                                            Matches
                                                                           Query Match
                                                                                                                Sequence
                                                                                                                                                                 for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention discloses a microarray comprising a plurality of acid probes including one of 2,018,500 fully defined sequences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New array of nucleic acid probes, useful for in Southern, Northern or dot-blot hybridization to sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4223; 9pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST; ss; probe; expressed sequence tag; microarray; genetic variation; biallelic marker; polymorphism; l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human microarray DNA oligonucleotide
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                                                              Local
                                                                                                                                                    USPTO at
4 CCATATTTATGGAATGA
                                            l Similarity
                                                                                                                  25
                                                                                                               BP; 6
                                            Conservative
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                                                                                                                                                seqdata.uspto.goc/sequence.html
                                                                                                               ð,
                                                         69.0%;
88.2%;
                                                                                                               6 C; 4
         20
                                                                                                               G; 9 T; 0 U; 0 Other;
                                            0
                                                           Score 13.8;
Pred. No. 5
                                            Mismatches
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                                                           .8e+03
                                                                               DB
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identify or detect
                                                                          Length
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Homo sapiens

WO2004076639-A2

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RESULT 14
AEA84363/c
ID AEA843
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clupus-affected or lupus-predisposed tissues as compared to disease-free cc tissues, a variant of the polypeptide and a polynucleotide encoding the clubus-gredisposed tissues as compared to disease-free cc tissues, a variant of the polypeptide and a polynucleotide encoding the cc polypeptide or variant. The invention also relates to detecting an cc subject and comparing the expression profile to a reference expression cc profile of the gene to detect or monitor an autoimmune disease in a cc subject, where the gene is differentially expressed in pre-symptomatic lupus-affected or lupus-predisposed tissues as compared to disease-free cc tissues, administering a therapeutically or prophylactically effective camount of the pharmaceutical composition in a subject, preferably a human cc ease in the cells before and after the contacting to determine if the capent modulates expression profiles or protein activities of at least come gene in the cells before and after the contacting to determine if the agent modulates expression or protein activities of at least one gene in the biological sample before and after the administering to determine if the least one gene in the subject, where the gene is differentially expressed cc disease-free kidney tissues. The pharmaceutical composition is useful for diagnosing, treating and preventing autoimmune diseases such as lupus repeated sinuman lupus-related sinum target sequence of the invention. Note: The cc muman lupus related sinum target sequence of the invention. Note: The cc sequence data for this patent did not form part of the protein activited.
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26-FEB-2003;
26-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New pharmaceutical composition comprising a polypeptide encoded by a that is differentially expressed in a pre-symptomatic lupus-affected predisposed tissues, and a carrier, useful for treating lupus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'toole
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(OTOO/)
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O'TOOLE M
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                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 6 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003US-0449693P.
2003US-0449753P.
2003US-0449795P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2004WO-US005655
                                                                                                                                                                                                                                                                                                                                               69.0%;
88.2%;
                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                  Score 13.8;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                     .7e+03
                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the printed
at directly from WIPO
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AEA84363 standard; cDNA; 21

ВP

Query Match
Best Local Similarity
Matches 15; Conserv

Conservative

0;

Mismatches

Indels Length

Gaps

0,

21; 0

69.0**%;** 88.2**%;** 

Score 13.8; DB 13; Pred. No. 5.7e+03;

21

σ A,

4 C; 4

G; 7

T;

U; 0 Other,

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CC carrier and at least one active component selected from a polypeptide concoded by a gene that is differentially expressed in pre-symptomatic cC lupus-affected or lupus-predisposed tissues as compared to disease-free ctissues, a variant of the polypeptide and a polynucleotide encoding the colypeptide or variant. The invention also relates to detecting an cc expression profile of at least one gene in a biological sample of a cc subject and comparing the expression profile to a reference expression cc subject, where the gene is differentially expressed in pre-symptomatic cc lupus-affected or lupus-predisposed tissues as compared to disease-free ctissues, administering a therapeutically or prophylactically effective camount of the pharmaceutical composition in a subject, preferably a human cc ease in the cells before and after the contacting to determine if the agent modulates expression profiles or protein activities of at least cone gene in the biological sample before and after the contacting to determine if the agent modulates expression or protein activities of at least one gene in the biological sample before and after the administering to determine if the agent modulates expression or protein activities of at least one gene in the biological sample before and after the administering to determine if the least one gene in the subject, where the gene is differentially expressed in lupus-affected or lupus-predisposed confidence in activities of at least one gene in the biological sample before and after the administering to determine if the least one gene in the subject, where the gene is differentially expressed in lupus-affected or lupus-predisposed subject confidence in activity of at least one gene in the subject, where the gene is differentially expressed in lupus-affected or lupus-predisposed subject.

CC disposing, treating and preventing autoimmune diseases such as lupus expressed in a lupus related slawn target sequence of the printed.
                                    sequence data for this patent did not form part of the specification, but was obtained in electronic format at ftp.wipo.int/pub/published pot sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2003; 2003US-0449693P
26-FEB-2003; 2003US-0449753P
26-FEB-2003; 2003US-0449795P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            predisposed tissues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New pharmaceutical composition comprising a polypeptide encoded by that is differentially expressed in a pre-symptomatic lupus-affecte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-662008/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'toole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMHP )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosis; genetic marker; autoimmune disease; systemic lupus erythematosus; lupus nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lupus-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2004; 2004WO-US005655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressive; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEA84363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (/TIEM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O'TOOLE M M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 9676; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          siRNA target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and a carrier, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lupus nephritis; nephritis;
ic; antiinflammatory; dermat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatological;
                                                             he printed directly be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lupus-affected
ng lupus.
                                                               from WIPO
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RESULT 11
AD774704/c
ID AD7747
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XX I CECEPT
XX I CECEPT
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                                                                                                                                   Query Match
Best Local (
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                        cytokine (TRANCE), osteoprotegerin ligand (OPGL), osteoclast differentiation factor (ODF) and TNFSF11. The present invention describes a screening method to identify potential therapeutic agents with osteopathic activity that can affect bone metabolism and are useful for the treatment or prevention of osteoporosis. As such, it refers to administering this agent to the mouse model and assessing the mouse for an alteration in a bone metabolism related marker such as RANKL. Furthermore, it describes a method for testing a mouse model for bone metabolism disease by administering an antisense oligonucleotide to modulate RANK or RANK or RANKL mRNA expression, and subsequently administering PTH to the mouse in order to assess the effect of the antisense oligo on the mouse compared to a control mouse treated with calcitonin. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Specifically, it refers to a mouse that is exposed to a compound selected from parathyroid hormone (PTH), its analogue or a fragment thereof, for a time sufficient to allow serum calcium concentration and the receptor activator of NFkappaB ligand (RANKL) mRNA expression to increase in the mouse model. Note that the RANKL gene maps to human chromosome 13q14 and is also known as tumor necrosis factor (TNP)-related activation-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New mouse model exposed to parathyroid hormone (PTH), its analog or fragment so that serum calcium concentration and RANKL mRNA expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor activator of NF-kappaB ligand; RANKL; metabolic bone disease; screening; osteopathic, antisense therapy; PCR; primer; ss.
                                                                                                                                                                                                                    Sequence 25
                                                                                                                                                                                                                                                                                                 oligonucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are increased, useful for screening agents osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-2003; 2003US-00667236.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2005060764-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GREG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADY74704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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20
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                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; SEQ ID NO 349; 101pp; English.
                                  CCCCATATTTATGGAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCCATATTTATGGA
                                                                                                                                                                                                                    BP;
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relates to novel mouse model for bone metabolism
                                                                                                                                                                                                                    6
                                                                                                                                                                                                                    A.
                                                                                                                                 71.0%;
84.2%;
                                                                                                                                                                                                                    2
C;
                                                                                                                                                                                                                                                                                                    is a PCR primer
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                                                                                                                                                                                                                    G.
                                                                                                          0
                                                                                                                                 Score 14.2; DB 14
Pred. No. 3.7e+03;
                                                                                                                                                                                                                    11 T; 0 U;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RANKL)
                                                                                                                                                                                                                                                                                                 given in an
                                                                                                                                                             DB 14;
                                                                                                                                                                                                                    0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        animal disease
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                                                                                                                                                          Length
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                                                                                                             Indels
                                                                                                                                                                                                                                                                                                    exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer Seq
                                                                                                                                                                25
                                                                                                       0;
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RESULT 13
AEA82113/c
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ADY97749/c
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Best Local Similarity
                                                                                                                                                                                                                                            Matches
                     Diagnosis; genetic marker; autoimmune disease; systemic lupus erythematosus; lupus nephritis; nephritis;
                                                                                                                                                                                                                                                                                                                                    The invention relates to a compound targeted to a nucleic acid molecula encoding RANKL which inhibits the expression of RANKL mRNA by at least 10%. The compound is useful in preparing a composition for treating or preventing a RANKL associated disease or condition in an animal, e.g., bone metabolism disease, osteoporosis, multiple myeloma, breast cancer related osteolysis, rheumatoid arthritis, collagen-induced arthritis or related osteolysis, rheumatoid arthritis, collagen-induced arthritis or
                                                                                  11-AUG-2005
                                                                                                          AEA82113
                                                                                                                               AEA82113 standard; cDNA;
                                                                                                                                                                                                                                                                                         Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                               New compound comprising 8 to 80 molecule encoding RANKL, useful or preventing a RANKL associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteopathic; antiarthritic; antirheumatic; antisense therapy; hematological disease; immune disorder; degeneration; endocrine musculoskeletal disease; inflammation; ss; PCR; primer.
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 23; SEQ ID NO 349; 259pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-2003; 2003US-0560750P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADY97749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADY97749 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-2004; 2004WO-US030736
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                                                                                                                                                                                                                                                                                                                             idjuvant-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                primer.
                                                         lupus-related
                                                                                                                                                                                            20
                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteoporosis;
                                                                                                                                                                                           CCCAACATTTATGGAATAA
                                                                                                                                                                                                                 CCCCATATTTATGGAATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bennett FC,
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                         BP; 6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      forward
                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                            arthritis.
                                                          SIRNA
                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry
                                                                                                                                                                                                                                                    71.0%;
84.2%;
                                                                                                                                                                                                                                                                                         2 C; 6 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                               associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer SEQ
                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dobie KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             გ
5
                                                        target sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΒP
                                                                                                                                                                                                                                         <u>,</u>
                                                                                                                               В₽
                                                                                                                                                                                                                                                                                                                         The present sequence represents a mouse
                                                                                                                                                                                                                                                    Score 14.2; DB 1
Pred. No. 3.7e+03
                                                                                                                                                                                                                                                                                         11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleobases targeted to a r in preparing a composition d conditions e.g. osteoporos
                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ζ,
                                                                                                                                                                                                                                                                 DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finger
                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                         Indels
           dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ċ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                  molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                           treating
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                             RANKI
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                    S
                                               Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antimicrobial; antiinflammatory; cytostatic; antisense therapy; superoxide dismutase; superoxide dismutase modulator; infection; inflammation; tunor; ss; gene expression; 2'-MOE; 2'-MOE wings; 2'-methoxyethyl; phosphorothioate.
                                                                                                                                    targeted to nucleobases 96-523 of a coding region of a nucleic acid molecule encoding human superoxide dismutase 1, soluble comprising 874 bp fully defined in the specification, where the compound specifically hybridizes with and inhibits the expression of human superoxide dismutase 1, soluble. The compound is useful for modulating of superoxide dismutase 2, soluble expression or for treating diseases associated with expression of superoxide dismutase 1, soluble. It can also be used to prevent or delay infection, inflammation, or tumor formation. This sequence corresponds to an antisense oligonucleotide targeted to the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat superoxide dismutase 1 gene antisense oligo #110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-2001;
04-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2005019915-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_base
                                                                                                                                                                                                                                                                                                                                                                             WPT; 2005-100832/11.
                                                                                                                                                                                                                                                                                                                                                                                                       Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2003; 2003US-00672866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_base
                                                                                                  Sequence
                                                                                                                                                                                                                                                          The invention relates to an antisense compound 8-50 nucleobases in length
                                                                                                                                                                                                                                                                                   Example 19; SEQ ID NO 271; 116pp; English.
                                                                                                                                                                                                                                                                                                                        treating
                                                                                                                                                                                                                                                                                                                                       the expression of
                                                                                                                                                                                                                                                                                                                                                   New antisense compound which specifically hybridizes with and inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                               (DOBI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (BENN/)
                                                            Local Similarity
                                                 15;
<sub>5</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                              BENNETT C F.
DOBIE K W.
                                                                                                                                                                                                                                                                                                                        ession of human superoxide dismutase 1, soluble, useful for diseases associated with expression of superoxide dismutase
                                                                                                   20
              TCCCCATATTTATGGA
TCCCCATATTGATGGA
                                                                                                                            dismutase 1 gene
                                                 Conservative
                                                                                                  BP; 5 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-00888360
2003US-00633843
                                                                                                                                                                                                                                                                                                                                                                                                    Dobie KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inkages. All C bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        base=
                                                          72.0%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      base= OTHER
== "2'-methoxyethyl nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internucleotide linkages are phosphorothioate
ll C bases are 5-methylcytidine bases"
                                                0
                                                                                                                             for inhibition of
                                                            Score
Pred.
                                                   Mismatches
                                                               ĕ
                                                                          14.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotides'
                                                              .9e+03
                                                                           DB 14;
                                                                                                                            gene
                                                   Indels
                                                                       Length
                                                                                                                            expression.
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                                                   0,
                                                   Gaps
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RESULT 10

Best Loc Matches

Local Similarity nes 15; Conser

Conservative

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Mismatches

Indels

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No.

2.9e+03

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ADW64179
ADW64179
AC ADW6
XX
AC A
                                                                                                                             The invention relates to an antisense compound 8-50 nucleobases in length targeted to nucleobases 96-523 of a coding region of a nucleic acid molecule encoding human superoxide dismutase 1, soluble comprising 874 bp fully defined in the specification, where the compound specifically hybridizes with and inhibits the expression of human superoxide dismutase 1, soluble. The compound is useful for modulating of superoxide dismutase 1, soluble expression or for treating diseases associated with expression of superoxide dismutase 1, soluble. It can also be used to prevent or delay infection, inflammation, or tumor formation. This sequence corresponds to an antisense oligonucleotide targeted to the rat superoxide dismutase 1 gene for inhibition of gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2'-methoxyethyl; phosphorothicate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antimicrobial; antiinflammatory; cytostatic; antisense therapy; superoxide dismutase; superoxide dismutase modulator; infection inflammation; tumor; ss; gene expression; 2'-MOB; 2'-MOB wings;
                                                                                 Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound which specifically hybridizes with and inhibits the expression of human superoxide dismutase 1, soluble, useful for treating diseases associated with expression of superoxide dismutase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2001;
04-AUG-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat superoxide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soluble
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BENNETT C F.
DOBIE K W.
                                                                                   BP; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dobie KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003US-00633843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dismutase 1 gene antisense oligo #108
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/note= "2'-methoxyethyl nucleotides"
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.inkages. All C bases are 5-methylcytidine bases"
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72.0%;
93.8%;
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                                                                                   C; 4
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ق
                                 Score 14.4; DB 14;
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deletions in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients own production of polypeptide. Additionally, (I) and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The polypeptides encoded by (I) may be used as antigens in the production of antibodies specific for polymorphic polypeptides. The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polymorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs). AAM53114 to AAM53329 represent peptides related to human polymorphic polynucleotide sequences. The sequences can be used in gene and protein therapy, and in vaccine production. (I) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. For example, (I) may be used to treat disorders by rectifying mutations or example.
antimicrobial; antiinflammatory; cytostatic; antisense therapy; superoxide dismutase; superoxide dismutase modulator; infection inflammation; tumor; ss; gene expression; 2'-MOE; 2'-MOE wings;
                                                                                                                                                        Rat superoxide
                                                                                                                                                                                                                                  07-APR-2005
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29-NOV-2000; 2000US-00726173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                dismutase 1 gene antisense oligo #109
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1476 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 9
ADW64181
ID ADW6
XX
AC ADW6
XX
DT 07-A
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                                                                                                                                   S
                                                                                                                                                                                                               Matches
                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                 targeted to nucleobases 96-523 of a coding region of a nucleic acid molecule encoding human superoxide dismutase 1, soluble comprising 874 bp fully defined in the specification, where the compound specifically hybridizes with and inhibits the expression of human superoxide dismutase 1, soluble. The compound is useful for modulating of superoxide dismutase 1, soluble expression or for treating diseases associated with expression of superoxide dismutase 1, soluble. It can also used to prevent or delay infection, inflammation, or tumor formation. This sequence corresponds to an antisense oligonucleotide targeted to the rat superoxide dismutase 1 gene for inhibition of gene expression.
 07-APR-2005
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense compound which specifically hybridizes with and inhibits the expression of human superoxide dismutase 1, soluble, useful for treating diseases associated with expression of superoxide dismutase 1,
                         ADW64181;
                                                  ADW64181 standard;
                                                                                                                                                                                                                                                                                                                                                            The invention relates to an antisense compound 8-50 nucleobases in
                                                                                                                                                                                                                                                                                                                                                                                      Example 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-100832/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennett CF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2001; 2001US-00888360
04-AUG-2003; 2003US-00633843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BENN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2005019915-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2'-methoxyethyl; phosphorothioate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOBIE K W.
                                                                                                              w
                                                                                                                                    -
                                                                                                                                                                         Similarity
                                                                                                                                TCCCCATATTTATGGA 16
                                                                                                                                                                                                             20
                                                                                                                                                              Conservative
                                                                                                                                                                                                             BP; 5 A;
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 270; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dobie
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003US-00672866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16. .20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mod base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inkages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mod base=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "all
                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ž
                                                                                                                                                                                                            5 C; 4 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                        93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _base= OTHER
e= "2'-methoxyethyl nucleotides'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 internucleotide linkages are phosphorothioate
All C bases are 5-methylcytidine bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -methoxyethyl
                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER
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                                                                                                                                                             0;
                                                                                                                                                                        Score 14.4; DB 14
Pred. No. 2.9e+03;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotides'
                                                                                                                                                                                     DB 14;
                                                                                                                                                                                  Length
                                                                                                                                                             0,
                                                                                                                                                             Gaps
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27-FEB-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC toxicological response to an agent, which comprises comparing the capression profile of one or more human toxic response genes to a cc reference gene expression profile indicative of toxicity, and so cc determining the presence of a toxic response to the agent. Also cc determining the presence of a toxic response to the agent. Also cc from the genes corresponding to the partial sequences given in ABZ82842 cc from the genes corresponding to the partial sequences given in ABZ82842 cc response gene plays a role on toxic response pathways by determining the cxpression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) cc expression profile to an agent; (b) obtaining the test gene expression profile corresponse gene plays a role on toxic response gene plays a role on toxic response gent, comprising: (a) cc exposing cells to an agent or isolating cells from a human subject who cc was exposed to an agent; (b) obtaining the test gene expression profile corresponse gene after exposure to a known toxic response gene after exposure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of that gene after comparing the test profile to the expression profile of that gene after comparing the test profile to the expression profile of that gene after compounds. The marrays comparing the test profile of a gene with a similar function or system level. The arrays comparising the human genes are useful for toxic cological servening to drugs, pharmaceutical compounds and chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 8 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 342; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-268322/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2002; 2002WO-US026514
                                                                                                                  plant protectant; fungicide; plant growth regulant; gene therapy;
cell cycle; gene expression; plant; transgenic plant; microarray;
                                                                                                                                                                                P. radiata
                                                                                                                                                                                                                         22-SEP-2005
                                                                                                                                                                                                                                                                 AEB27395;
                                                                                                                                                                                                                                                                                                       AEB27395 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2001; 2001US-0313080P
                   WO2005065339-A2
                                                           Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCATATTTATGGAATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                            CCCAATATTTATGGAAGGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn RT,
                                                                                                                                                                              cell cycle gene microarray oligo SEQ ID NO 556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention describes a method
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adkins K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%;
                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pickett GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (M1) for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kier LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schmeiser
                                                                                                                       microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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AAI78770/c
ID AAI787
XX
AC AAI787
XX
OF 09-NOV

AAI78770 standard; DNA; 51

09-NOV-2001 AAI78770;

(first entry)

밁 Ś

53  $\vdash$ 

TCCCCAAACTTATGGAAAGA 34 TCCCCATATTTATGGAATGA 20

0,

RESULT 7

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CC sequence or SEQ ID NOS: 1-23/ OF INDSTRAIL COMBETVALIAL SITE AND CC polypeptide of SEQ ID NOS: 261-497, where the polymurlectide encodes a complete of SEQ ID NOS: 261-497 and comparison of SEQ ID NOS: 261-497 and comparison of SEQ ID NOS: 361-497 and comparison of SEQ ID NOS: 471-697. Also described care: (1) a DNA construct comprising at least one polymurlectide having the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a comparison of SEQ ID NOS: 471-697. Also described the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a comparison of SEQ ID NOS: 1-237 or their conservative variants; (2) a comparison of SEQ ID NOS: 1-237 or their conservative variants; (2) a comparison of making wood or wood pulp obtained from a transgenic comprising an amino acid sequence encoded by the new isolated comprising an amino acid sequence encoded by the new isolated (1); (6) a comparison of an method of correlating gene expression in two different samples; (1) a method of correlating gene expression of a plant phenotype of a plant; (9) combination, for detecting expression of a plant phenotype to the level of comparison of a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene expression in the plant of one or more genes; (11) a method of correlating the combination of the cell cycle; (12) a combination, for detecting expression of a plant phenotype to the level of comprising the combination of (12) provided on a solid conscravay comparising the combination of (12) provided on a solid conscravay comparising the combination of (12) provided on a solid conscravay comparison, comparison of conserving one or more nucleic acid sequence of SEQ ID NOS: 1-237; (13) a conscravay construct, composition, comparison of the cell cycle and (16) a kit, for cell cycle and methods are useful for modelypeptides, DNA construct, composition, comparison the microarray of the cell cycle enes.

CC and methods are useful for modelypeptides, DNA construct, composition, comparison the microarray for detecting one o
Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 43; SEQ ID NO 556; 499pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide encoding a plant cell modifying plant development and altering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-2004; 2004WO-US043804
                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2005
l Similarity
17; Conserv
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GENESIS RES
                                                                                                                                       60
                                                                                                                                BP; 14
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Connett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    describes an isolated polynucleotide comprising: (i) a EQ ID NOS: 1-237 or their conservative variants; (ii) a
                                                                                                                                       P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  & DEV CORP LTD
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Kodrzycki RJ;
                                      76.0%;
85.0%;
                                                                                                                                       12
                                                                                                                                       C; 13 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emerson SJ,
      ..
                                      Score 15.2;
Pred. No. 1.
             Mismatches
                                                                                                                                          21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grigor MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cycle protein, useful plant phenotype.
                                         3e+03
                                                                     DB 14;
                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Higgins
                                                                            60;
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             0
             Gaps
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RESULT 3
ADN49091/c
ID ADN49091 standard; DI
XX ADN49091;
XX
AC ADN49091;
XX
DT 15-JUL-2004 (first of the context of the conte
    RESULT 4
ADM49066
ID ADM4
XX ADM4
XX ADM4
XX ADM4
XX BE Huma
XX Hist
XX Hist
XX Hist
XX Hist
XX ADM4
XX Hist
XX Hype
XX Homc
OS Synt
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                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense compounds, compositions and methods for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 is also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition comprises antisense compounds that can be targeted towards HDAC2. The compound is useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer. It is also useful in antisense gene therapy. The present sequence is human HDAC2 DNA target region. Human HDAC2 gene is located at chromosome 6q21.
                                                                          Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3; hyperproliferative disorder; cancer; antisense gene thera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New compound, having a sequence targeted to a coding region of a nucleic acid encoding human histone deacetylase 2, useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer.
                                                            antisense;
                                                                                                                                         Human
                                                                                                                                                                                                                    ADN49066;
                                                                                                                                                                                                                                                         ADN49066 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2002; 2002US-00173192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histone deacetylase 2; HDAC2; HDAC-2; hdca2; RPD3; hRPD3; hyperproliferative disorder; cancer; antisense gene there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-340037/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human histone deacetylase 2
                                                                                                                                         HDAC2
                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                          TCCCCATATTTATGGAATGA 1
                                                                                                                                                                                                                                                                                                                                                                                  TCCCCATATTTATGGAATGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dobie KW
                                                            phosphorothicate backbone;
                                                                                                                                     specific antisense oligo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 7 A; 3 C; 4 G; 6 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 62; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                       ISIS 157268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 Other;
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                                                                            therapy; human;
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RESULT 5
ABZ84349
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Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to antisense compounds, compositions and methods for modulating the expression of histone deacetylase 2 (MDAC2). HDAC2 also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition comprises antisense compounds that can be targeted towards HDAC2. The compound is useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer. It is also useful in antisense gene therapy. The present sequence is an antisense oligonucleotide targeted to human HDAC2 DNA.
Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New compound, having a sequence targeted to a coding region of a nuc acid encoding human histone deacetylase 2, useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer.
                                                   Toxicologically
                                                                                     Toxicologically
                                                                                                                        14-MAY-2003
                                                                                                                                                           ABZ84349;
                                                                                                                                                                                             ABZ84349 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                   TCCCCATATTTATGGAATGA
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                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;
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¥ P
                                                                                     relevant human
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/mod_base= (
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/note= "Phosphorothioate backbone in which all cytidines
are 5-methylcytidines"
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100.0%; Pred.
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                                                   toxicological response;
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                                                                                     primer #1508.
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RESULT 1
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                                                                                                                                                                                  The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder. The invention is also useful in antisense-therapy. The present sequence is human histone deacetylase 2 target DNA fragment used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperproliferative disorder; cancer; apoptosis; metabolic antisense-therapy; cytostatic; antiinflammatory; human; de
                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotide compound, useful for diagnosing, preventing and/or treating conditions with aberrant activity of the histone
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                                                                                                        Similarity
                                                         TCCCCATATTTATGGAATGA 20
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63.0
63.0
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                                                                                                                                                                                                                                                                                                                                                                                                     2, such as cancer, inflammation and metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deacetylase 2 target DNA
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                                                                                                        100.0%;
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ADM88089
AAZ29013
AAZ29010
AEA10339
AAX95057
ADT00674
ADU74605
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Pred.
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                                                                                                          4.8;
                                                                                                                                                       0 Other;
                                                                                                                       DB 12; Length 20;
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                                                                                            Indels
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Aax95057 PCR prime
Adt00674 Novel mut
Adu74605 Saccharom
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Aaz29013 5' primer
Aaz29010 Amplified
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RESULT 2 ADJ27020

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The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder. The invention is also useful in antisense-therapy. The present sequence is human histone deacetylase 2 DNA antisense oligonucleotide used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense oligonucleotide compound, useful for diagnosing, p and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperpoliferative disorder; cancer; appolosis; metabolic disorder; antisense-therapy; cytostatic; antiinflammatory; human; phosphorothioate backbone; antisense; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 15; SEQ ID NO 37; 46pp; English.
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                                                                                                                                                                             Sequence
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                                                                                                              Similarity
                                 TCCCCATATTTATGGAATGA
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TCCCCATATTTATGGAATGA 20
                                                                                                                                                                             BP; 6 A; 4 C; 3 G; 7 T;
                                                                                        Conservative
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/mod_base= OTHER
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'note= "Phosphorothioate
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                                                                                                         100.0%; Score 20; DB 100.0%; Pred. No. 4.8;
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                                                                                                                                    Length
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Minimum
Maximum
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Perfect
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Adw64179 Rat super
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Ady74704 Receptor
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Aea84363 Human lup
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Ads 92006 DNA oligo
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Adb 99305 PCR prime
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Adb 9107 Human Cdk
Adb 9107 Human Cdk
Adb 9107 Human Spl
Adw 9166 Human Cdk
Adb 9107 Human D04
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Homo sapiens
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Sequence 1 from Patent W003101985.
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AX960556.1 GI:40880613
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Homo sapiens
Eukaryota, Ketazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                                                                                                                                                                                                 2-oxo-1,3,4-trihydroquinazolinyl derivatives for the treatment ofcell proliferation-related disorders Patent: WO 03101985-A 1 11-DEC-2003; Amgen Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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and Zhong,W.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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Sequence 791 from Patent WO02053728.
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Detection of genetic polymorphisms
Patent: WO 02052044-A 7433 04-UUL-2002;
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AX816400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                    /mol_type="unassigned
                                                                                                                                                                                                                  /organism="unknown"
                       from Patent W003066630.
                                                                                                                                                                                                                                                                                                                                                    GI:20240668
                                                                                                                                                       66.0%;
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Pred. No. 2.1e+05;
                                                                                                                                             Score 13.2; DB 6;
Pred. No. 2.1e+05;
0; Mismatches 3;
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CQ903062
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Sequence
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Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria;
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                       CQ903062
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Protein-protein interactions in Helicobacter
Patent: WO 02066501-A 5058 29-AUG-2002;
Hybrigenics (FR); INSTITUT PASTEUR (FR)
                                                                                                                                                                                                                                                                                                                                                                             Sequence 5058 from Patent AX792594
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Glycine max
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Sequence 1027 from Patent
AX197320
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Patent: WO 0151627-A 1027 19-JUL-2001;
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                                                                                                                                                                                                                                                                                                           Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                     /organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="unassigned DNA"
/db_xref="taxon:3847"
/note="Seq ID: 515002_region_G2.
                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No. 2.2e+05;
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Pred. No. 2.3e+05;
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WO0151627.
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AR119628/c
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AR169109
AR169109.1
                                   1 (bases 1 to 38)
Wisnewski, N., Silver, G.M., Lo, K. Callies.
Anti-flea epoxide hydrolase antibodies an
Patent: US 6290958-A 17 18-SEP-2001;
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Sequence
AR119628
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Wisnewski, N., Silver, G.M., Lo, K. Callies.
Flea epoxide hydrolase proteins and uses
Patent: US 6153397-A 17 28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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                                                                                         Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.
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                        Location/Qualifiers
organism="unknown"
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/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                  s. and Brandt, K.S.
and uses thereof
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1 (bases 1 to Sukhatme, V.P.
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Sequence
AR014537
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Sukhatme, V.P.
Methods and materials relating to the functional domains of binding proteins
Patent: US 5763209-A 45 09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3251 from Patent CS013326 CS013326.1 GI:59673141
                                                                                                                                                                                                                                                                                                                                                                                                                                                         binding proteins Patent: US 5773583-A 45 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methods and materials relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
                                                                                           Hakonarson, H., Gurney Methods of diagnosis
                                                                                                                                                                   Homo sapiens
                                                         Patent: WO 2005007144-A 3251
Decode Genetics EHF. (IS)
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                              Homo sapiens (human)
                                                                                   association
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ilarity 83.3%;
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/mol_type="unassigned
                                             netics EHF. (IS)
Location/Qualifiers
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/mol_type="unassigned DNA"
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/mol_type="unassigned DNA"
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Pred. No. 2.4e+05;
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TGF-beta hybrid PCR
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AL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gastron Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

S. iocation/Qualifiers
Sequence 5712 1
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AX162384.1 GI:
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Sequence 859
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                                         AX162384
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Blumenfeld, M., Chu
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                                                                                                                                                                                                                                 /organism="unknown"
/mol_type="genomic DNA"
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left border"
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/clone_lib="Arabidopsis thaliana T-DNA
/ecotype="Wassilewskija"
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Pred. No. 1.7e+05;
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Unclassified.
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Patent: US 6300132-A 56 09-OCT-2001;
Isis Pharmaceuticals, Inc.; Carlabad,
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Patent:
                                                 AR012098.1
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Monia, B.P. and Cowsert, L.M.
Antisense inhibition of telomeric repeat binding factor 2
                       Unknown.
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Mammalia; Eutheria;
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Accession number cg44023776"
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from patent US 5763209
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Brucella melitensis biovar Abortus
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                                                                                                                                                                                                                   2 (bases 1 to 75)
Hematti,P., Hong,B.-K., Ferguson,C.,
Dunbar,C.E. and Calmels,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                      Hematti,P., Hong,B.K., Ferguson,C., Adler,R., Hanawa,H., Sellers,S., Holt,I.E., Eckfeldt,C.E., Sharma,Y., Schmidt,M., Kalle,C., Persons,D.A., Billings,E.M., Verfaillie,C.M., Nienhuis,A.W., Wolfsberg,T.G., Dunbar,C.E. and Calmels,B. Distinct genomic integration of MIV and SIV vectors in primate hematopoietic stem and progenitor cells places and places and places are places and places are places and places and places are places and places are places and places and places are places and places and places are places are places are places and places are places a
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DNA drives expression of luciferase in B.
tryptose and erythritol but not glucose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brucellaceae; Brucella.
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                                                                                                                            Submitted (19-AUG-2004) Hematology Drive, Bethesda, MD 20892, USA Location/Qualifiers
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/strain="2308"
/db_xref="taxon:235"
/organism="Macaca mulatta"
/mol type="genomic DNA"
/isolate="SIV_RQ3556_6p21.32c"
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Sequence 348 from Patent
CS010423
CS010423.1 GI:59670238
                                          of pre-insertion sites EMBO Rep. 3 (12), 1152
                                                                     Lepiniec,L., Caboche,M. and Lecharny,A. T-DNA integration into the Arabidopsis
                                                                               Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F. Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Decode Genetics EHF. (IS)
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Mammalia; Eutheria;
2 (bases 1 to 42)
Balzergue, S.
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/cell_type="circulating
cells"
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/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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Pred. No. 1.2e
0; Mismatches
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Pred. No. 1.8e+05;
0; Mismatches 1
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WO2005007144.
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A flanking
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KEYWORDS
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CQ814459/c
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AUTHORS
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AX791547/c
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                                                                                                                                                                                                                                                Kauppinen,S., Alsbo,C., Nielsen,P.S., Jeffares,D.C., Mourier,T., Arctander,P., Tommerup,N., Tolstrup,N. and Vissing,H. Oligonucleotides useful for detecting and analyzing nucleic acidsof
                                                                                                                                                                                                                                                                                                                                                                  CQ814459
Sequence 820 from Patent
CQ814459
CQ814459.1 GI:47603663
                                                                                                                                                                                                             Patent: WO 2004035819-A 820 29-APR-2004; Exigon A/S (DK)
                                                                                                                                                                                                                                                                                                                         synthetic construct synthetic construct
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Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Sequence 4011 from Patent
AX791547
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                                                                                                                                                                                                                                                                                                            other sequences; artificial sequences.
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                                                                    Similarity
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                TCCCCATATTTATGGAATGA 20
TTCACATATTTATCGATTGA 15
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                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                       /organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="Synthetic oligonucleotide
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Helicobacter pylori"
/mol_type="unassigned DNA"
/db_xref="taxon:210"
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                                                                80.0%;
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84.2%;
                                                   Score 13.6; DB 6;
Pred. No. 1.4e+05;
0; Mismatches 4
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Pred. No. 1.4e+05;
0; Mismatches 4;
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Pred. No. 6.4e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                              40 bp DNA
WO2004035819.
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WO02066501.
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RESULT 8
AF072570/c
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CQ557319
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CQ814451/c
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TITLE
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Best Local Similarity 80.0%;
Matches 16; Conservative
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                                                                                       1 TCCCCATATTTATGGAATGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ557319 6
Sequence 26954 from Patent CQ557319 CQ557319.1 GI:41523746
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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Sequence 812 from Patent
CQ814451
CQ814451.1 GI:47603655
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                                                                      TCCTCATATTTCTGGAGTCA
                                                                                                                                 Conservative
                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="unassigned DN/
/db_xref="taxon:1000"
                                                                                                                                                                                                                                                                  Location/Qualifiers
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/db_xref="taxon:32630"
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Pred. No. 1.3e+05;
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Pred. No. 1.3e+05;
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WO2004035819.
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AX162383/c
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DEFINITION
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VERSION
KEYWORDS
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AL807567
                     JOURNAL
REFERENCE
AUTHORS
TITLE
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Matches 15
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                                                                                  AUTHORS
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AX162383
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX162383.1 GI:14543714
          Direct Submission
Submitted (27-JUN-2002)
Lane, Norwich, NR4 7UJ,
                                                                                                                                  STS: STS, sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                tagged site.
AL807567
AL807567.1 GI:21628283
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Arabidopsis thaliana transposon
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                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                           Clarke, J.H.
                                                            Unpublished
                                                                        Murphy, G.,
                                                                                Clarke, J.H.,
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                                                    (bases 1 to 68)
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WO 0140521-A 5711 07-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                         /note="1 of 2 allelic variants
Accession number cg44023776"
                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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                                                                        Langham,
                                                                                Bowles, B.,
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Pred. No.
                                                                       , Carter,J., Hart,D., McCullagh,B., LeGrys,C., Jones,J.D.G. and Bevan,
              Clarke
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Best Local
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                    tagged site.
AL834013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     code: N105973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. 3 denotes a sequence derived from the 3'end of the transposon, 5 denotes a sequence derived from the 5'end of the transposon BBSRC GARNet, ATIS project
                                                                                                                                                                                                                                                                                   Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a grap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. 3 denotes a sequence derived from the 5'end of the transposon, 5 denotes a sequence derived from the 5'end of the transposon BESRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
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STS; STS; sequence tagged site.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Submitted (11-JUL-2002)
Lane, Norwich, NR4 7UJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 bp Arabidopsis thaliana transposon tagged site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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/clone="AC002328"
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Pred. No. 6.5e+04;
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AL807567

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CQ814451

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AR370235

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APPLICANT: Khoorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
INTERPORT MATSHALL William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirnA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR FILING DATE: 2003-11-4
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2003-19-10
PRIOR PILING DATE: 2003-11-4
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APPLICANT: Khvorova, A
APPLICANT: Reynolds, A
APPLICANT: Leake, Devi
APPLICANT: Marshall, V
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SEQ ID NO 1463744
LENGTH: 19
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Best Local Similarity
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Publication No. US20050246794A1
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TYPE: RNA
ORGANISM: Homo sapiens
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Reynolds, Angela
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Pred. No. 9e+02;
3; Mismatches 3;
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1066281
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               Search completed: March
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
Job time : 498.333 secs
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                                                                                                                                                                                                                                                        SOFTWARE: Proprietary SEQ ID NO 1066281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1066281, Application US/11083784 Publication No. US20050245475A1
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Best Local Similarity 83.3%;
                                                                                                                            Matches
                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1591911
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                                                                                          3 ATGGAATGATACCGTCAT 20
                                                                                                                                              Similarity
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                                                              AAGGAAAGAUACAGUCAU 18
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Reynolds, Angela
Leake, Devin
                                                                                                                            Conservative
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66.7%;
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Pred. No. 9e+02;
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Pred. No. 9e+02;
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                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et
                                                                                                                                                                                                        Sequence 30250, Application US/11175859
Publication No. US20060024715A1
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 293123
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILLING DATE: 2005-05-26
PRIOR FILLING DATE: 2005-05-26
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             CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
                                                                                                             APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
SOFTWARE:
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CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial
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TYPE: DNA
ORGANISM: Artificial
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PatentIn version 3.2
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Pred. No. 7.4e+02;
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Pred. No. 7.4e+02;
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US-11-101-244-1066281 Application U; Sequence 1066281, Application U; Publication No. US20050246794A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-11-101-244-605119
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SOFTWARE: Proprietary
SEQ ID NO 1066281
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Best Local Similarity
                                                FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
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                                                                                                                                                                          APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
ATTLE OF INVENTION: Functional and Hyperfunctional sirNA
                                                                                                                                                                                                                                                                      APPLICANT: Dharmacon, APPLICANT: Khvorova,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
                                 NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                   APPLICANT:
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SOFTWARE: Proprietary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
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Reynolds, Angela
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83.3%;
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82.4%;
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Pred. No. 96
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Pred. No. 8.6e+02;
1; Mismatches 2
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9e+02;
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US-11-121-849-649841
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; ORGANISM: Homo sapien
US-11-121-849-649079
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US-11-121-849-649842
                                                                                                         ; ORGANISM: Homo sapien 
US-11-121-849-649842
                                                                                                                                                      TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1 CURRENT APPLICATION NUMBER: US/11/121,849 CURRENT FILING DATE: 2005-05-03 PRIOR APPLICATION NUMBER: 60/567,949 PRIOR APPLING DATE: 2004-05-03 PRIOR PILING DATE: 2004-05-03 NUMBER: OF SEQ ID NOS: 673904 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 649842 LENGTH: 25
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SEQ ID NO 649079
LENGTH: 25
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Best Local
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Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity 93.3%;
                                                         Query Match
Best Local Similarity
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
FILE REFERENCE: 3684.1
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                             TYPE: DNA
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            TTATGGAATGATACC
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93.3%;
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Pred. No. 7.4e+02;
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Pred. No. 7.4e+02;
0; Mismatches 1
                                           Score 13.4; DB 12;
Pred. No. 7.4e+02;
0; Mismatches 1;
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US-11-136-527-26188/c
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          ; Sequence 293095, Application US/11136527; Publication No. US20050287570A1; GENERAL INFORMATION:
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US-11-136-527-26191/c
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                                                            RESULT 23
US-11-136-527-293095
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                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Probe US-11-136-527-26191
                                                                                                                                                                                                                                                                                             SEQ ID NO 26191
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial
FEATURE:
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Matches
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3
APPLICANT: Wyeth
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ORGANISM: Artificial
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APPLICANT: MOUNTS, William M
TITLE OF INVENTION: Probe Arrays For Express
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILLING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
ROPTMAND: DATE: T-
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26191, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: MOUNTS, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
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93.3%;
                 67.0%;
93.3%;
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Score 13.4; DB 12;
Pred. No. 7.4e+02;
0; Mismatches 1;
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Pred. No. 7.
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Sequence 1019090, Publication No. U

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US-11-083-784-1019090
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1019090
                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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APPLICANT: Khvorova, A
APPLICANT: Reynolds,
APPLICANT: Leake, Devi
APPLICANT: Marshall, W
APPLICANT: Scaringe, S
                                                                                                                Query Match
                                                                            Matches
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SEQ ID NO 1019090
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Best Local Similarity 66.7%;
Matches 10; Conservative
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
APPLICANT: Leake, Devin
                                                                                                                                                                                          LENGTH: 19
TYPE: RNA
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APPLICANT: Scaringe, Stephen
APPLICANT: Scaringe, Stephen
BITLE OF INVENTION: Functional and Hyperfunctional siRNA
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                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                              Local
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                                  6 GAATGATACCGTCAT 20
                                                                                              Similarity
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Leake, Devin
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Reynolds, Angela
Leake, Devin
                                                                          Conservative
                                                                                          67.0%;
66.7%;
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                                                                                        Score 13.4; DB 11
Pred. No. 6.9e+02;
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Pred. No. 6.9e+02;
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RESULT 16

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RESULT 18
US-11-121-849-649079
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; ORGANISM: Homo sapien
US-11-121-849-649078
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          Sequence 649079, Application US/11121849
Publication O. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2004-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION UMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
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CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 649077
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Publication No. US20050272080A1
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
NUMBER OF SEQ ID NOS: 673904
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Pred. No. 7.4e+02;
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Pred. No. 7.
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RESULT 10
US-11-175-859-108552/c
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US-11-121-849-550185/c
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; ORGANISM: homo sapien
US-11-175-859-108552
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APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et
                                  TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays

FILE REFERENCE: 3684.1 Microarrays

CURRENT APPLICATION NUMBER: US/11/121,849

CURRENT FILING DATE: 2005-05-03

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR APPLICATION NUMBER: 60/567,949

PRIOR FILING DATE: 2004-05-03

NUMBER OF SEQ ID NOS: 673904

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 550185

LENGTH: 25
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Best Local
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publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
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CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
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CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
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TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: homo sapien
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ORGANISM: Homo sapien
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      RESULT 14
US-11-101-244-1019090
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SEQ ID NO 83366
SEQ ID NO 83366
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-83366
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Publication No. US20060024715A1
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Best Local Similarity
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Publication No. US20060024715A1
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Best Local
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APPLICANT: Liu, Guoying et al.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
PRIOR FILING DATE: 2004-07-02
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CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
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PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
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TYPE: DNA
ORGANISM: homo sapien
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                                                                                    Similarity
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TCAATGAATGATACCATCAT 21
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80.0%; Pred. No. 6.7
tive 0; Mismatches
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                                                                  Score 13.6; DB 12;
Pred. No. 6.7e+02;
0; Mismatches 4;
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Pred. No. 5.7e+02;
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US-11-121-849-481834
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US-11-121-849-481834/c
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US-11-083-784-222605
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                                                                                                                                                                                                                                                                             Sequence 481834, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 222605
Query Match
Best Local Similarity
                                                                                                                SEQ ID NO 481834
LENGTH: 25
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Best Local (
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                                                                                                                                                                FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
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                                                                                                                                                 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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APPLICANT: Khvorova,
APPLICANT: Reynolds,
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TYPE: RNA
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional
                                                                         ORGANISM: Homo sapien
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                                                                                                TYPE: DNA
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84.2%;
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 Score 14.2; DB 12
Pred. No. 2.6e+02;
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PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
SEQ ID NO 35121
LENGTH: 50
TYPE: DNA
ORGANISM: homo Bapien
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                                                               Query Match
Best Local S
Matches 16
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PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence I
SEQ ID NO 621659
                                                                                                                                                                                                                                                                                                                                                        Sequence 35121, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
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APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
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CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
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                                                             71.0%; Score 14.2; DB 12; 84.2%; Pred. No. 3.1e+02; tive 0; Mismatches 3;
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Pred. No. 2
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US-11-175-859-31104

Sequence 31104, Application US/11175859 Publication No. US20060024715A1 GENERAL INFORMATION:

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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 222615
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APPLICANT: Khvorova, A
APPLICANT: Reynolds, A
APPLICANT: Leake, Devi
APPLICANT: Marshall, W
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SEQ ID NO 222615
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
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US-11-121-849-341700

US-11-121-849-343227

US-11-121-849-348164

US-11-121-849-371845

US-11-121-849-50186
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341700,
343227,
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APPLICANT: CONNETT, MARIE B.
APPLICANT: CONNETT, MARIE B.
APPLICANT: EMERSON, SARAH JANE
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: HIGGINS, COLLEEN M.
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: MAGUSIN, ANDREAS
APPLICANT: MODRZYCKI, BOB
TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
FILE REFERENCE: 044463-0360
CURRENT APPLICATION NUMBER: US/11/024,959
CURRENT APPLICATION NUMBER: 60/533,036
PRIOR APPLICATION NUMBER: 60/533,036
PRIOR APPLICATION NUMBER: 3003-12-30
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; ORGANISM: Eucalyptus sp.
US-11-024-959-556
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         SOFTWARE: Proprietary
SEQ ID NO 222605
LENGTH: 19
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Matches 18; Conserv
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                                                                                                 APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
                                                              PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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Similarity 90.0%;
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Reynolds, Angela
Leake, Devin
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No. 1:
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1: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq1:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq3:*
13: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq4:*
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78-11-121-849-62185
78-11-175-859-35121
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Sequence 31104,
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| US-11-136-527-2930250
| US-11-1063-784-1066281
| US-11-101-244-1066281
| US-11-101-244-1066281
| US-11-1083-784-1066281
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| US-11-1083-784-1066281
| US-11-1083-784-1066281
| US-11-101-244-1045281
| US-11-136-127-130459
| US-11-136-127-130459
| US-11-136-127-130459
| US-11-136-127-130471
| US-11-138-149-13044820
| US-11-136-144-1304820
| US-11-131-138-1362
| US-11-131-134-13640
| US-11-131-134-1
Sequence 1066281, Sequence 605119, Sequence 605119, Sequence 371442, Sequence 371427, Sequence 371427, Sequence 371427, Sequence 130458, Sequence 130459, Sequence 130471, Sequence 130474, Sequence 130474, Sequence 130474, Sequence 130474, Sequence 130479, Sequence 130479, Sequence 130479, Sequence 25870, A Sequence 57813, A Sequence 57813, A Sequence 57813, A Sequence 57813, A Sequence 7781, A Sequence 7781, A Sequence 78131, A Sequence 78131, A Sequence 78131, A Sequence 21012, A Sequence 21012, A Sequence 21012, A Sequence 21031, Sequence 21032, Sequence 21032, Sequence 21032, Sequence 21032, A Sequence 21034820, Sequence 21032, A Sequence 1044820, Sequence 1044820, Sequence 1044820, Sequence 1044820, Sequence 1044820, Sequence 81159, A S
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                                                                                  ; ORGANISM: Mus musculus 
US-10-719-900-606555
                                                                Query Match
                                               Matches
                                                        Local
             22
                                               16;
                            1 TTATGGAATGATACCGTCAT 20
             TTAGGAAATGATACTGTAAT 3
                                            0,
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CURRENT APPLICATION NUMBER: US/11/033,489
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 10/465,789
PRIOR APPLICATION NUMBER: 60/536,281
PRIOR APPLICATION NUMBER: 60/536,281
PRIOR PILING DATE: 2004-01-13
PRIOR PILING DATE: 2004-01-13
PRIOR PILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 136
SOFTWARE: PATENTE: 38
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
US-10-719-900-606555/c
US-10e-606555, Application US/10719900
; Publication No. US20050026164A1
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                                                                                                                                           APPLICANT: Xue Mei Zhou

APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 606555

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bayburt, Timothy H
APPLICANT: Schuler, Mary A
APPLICANT: Civjan, Natanya R
APPLICANT: Grinkova, Yelena V.
APPLICANT: Benisov, Ilia G.
APPLICANT: Grimme, Stephen G.
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00B
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Bayburi
APPLICANT: Schule:
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Local Similarity 88.2%;
les 15; Conservation
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h 68.0%; Score 13.6; DB 8; Length 25; Similarity 80.0%; Pred. No. 7e+03; 16; Conservative 0; Mismatches 4; Indels
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Pred. No. 6.6e+03;
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Search completed: March
Job time: 619.333 secs
                                                                                                                                                                                                                                                                ; ORGANISM: Probe Sequence US-10-956-157-211298
                                                                                                                                                                                                                                                                                                                          APPLICANT: Wyeth
APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: Mounts, WICLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITTITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION WIMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOCTWARE: PATENTIN VERSION 3.2
SEQ ID NO 211298
LENGTH: 25
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Publication No. US20050118625A1
GENERAL INFORMATION:
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Best Local S
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                                                                                       23 TTAGGGAAAGATACCAACAT 4
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l Similarity 80.0%;
16; Conservative
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                      1, 2006, 23:22:50
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Pred. No. 7e+03;
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INFORMATION:

Application US/11033489

US20050182243A1

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CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 10/465,789
PRIOR FILING DATE: 2003-06-18
PRIOR FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 60/536,281
PRIOR FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3
SEQ ID NO 65
LENGTH: 66
TYPE: DNA
ORGANIEM: Artificial Sequence
                                    Matches
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Publication No. US20040018530A1
                                                      Query Match
Best Local &
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PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/470,750
PRIOR APPLICATION NUMBER: 60/470,750
PRIOR FILING DATE: 2003-05-15
NUMBER OF SEC.
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APPLICANT: Mendonsa, Shaun D
TITLE OF INVENTION: IN VITRO EVOLUTION OF FUNCTIONAL RNA AND DNA USING
TITLE OF INVENTION: ELECTROPHORETIC SELECTION
FILE REFERENCE: 110.01870101
CURRENT APPLICATION NUMBER: US/10/448,250
CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy H
APPLICANT: Schuler, Mary A
APPLICANT: Civjan, Natanya R
APPLICANT: Grinkova, Yelena V.
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                                                                                                                                                                      ORGANISM: ARTIFICIAL SEQUENCE
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OTHER INFORMATION: sequence encoding Helix
                                                                                                                                                                                                              ENGTH: 80
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4 TGGAATGATACCGTCAT 20
                                                      Similarity
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Denisov, Ilia G.
                                      Conservative
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88.2%;
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                                                    Score 13.8; DB 7;
Pred. No. 6.6e+03;
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Pred. No. 6.4e+03;
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; OTHER INFORMATION: synthetic oligonucleotide
US-10-979-506-38
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US-10-465-789A-38
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US-10-465-789A-38/c
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
LENGTH: OF SEQ ID NO 38
                                                                            Query Match
Best Local :
                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy H
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00C
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/10465789A Publication No. US20040053384A1
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/979,506
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 87-00A
CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT FILING DATE: 2003-06-18
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APPLICANT: Schuler, Mary A
APPLICANT: Civjan, Natanya R
APPLICANT: Yelena V. Grinkova
APPLICANT: Ilia G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy
                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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nes 15; Conserv
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3 ATGGAATGATACCGTCA 19
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                                                                              Similarity
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                                                         Conservative
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88.2%;
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Pred. No. 6.6e+03;
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Pred. No. 6.6e+03;
                                                         Mismatches
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APPLICANT: Ilia G. Denisov
TITLE OF INVENTION: Membrane Scaffold Proteins

Civjan, Natanya R Yelena V. Grinkova

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RESULT 21
US-10-979-506-32
; Sequence 32, Application US/10979506
; Publication No. US20050152984A1
; Publication No. US20050152984A1
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                                                                     US-11-033-489-32
Sequence 32, Application US/11033489
Publication No. US20050182243A1
GENERAL INFORMATION:
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APPLICANT: Bayburt, Timothy H
TITLE OF INVENTION: Membrane Scaffold Proteins
FILE REFERENCE: 87-00C
CURRENT APPLICATION NUMBER: US/10/979,506
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 46
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SEQ ID NO 32
LENGTH: 54
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Matches
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SEQ ID NO 32
LENGTH: 54
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APPLICANT: Sligar, Stephen G
APPLICANT: Bayburt, Timothy H
APPLICANT: Schuler, Mary A
APPLICANT: Civjan, Natanya R
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CURRENT APPLICATION NUMBER: US/10/465,789A
CURRENT FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 09/990,087
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,233
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 89
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ORGANISM: Artificial Sequence
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Local Similarity 88.2%;
1es 15; Conservaring
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                 69.0%; Score 13.8; DB 9; 88.2%; Pred. No. 6.2e+03;
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Pred. No. 6.2e+03;
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                                                                                                                                               OTHER INFORMATION: sequence encoding Helix 4 US-10-465-789A-65
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PRIOR FILLING DATE: 2001-11-20
PRIOR PELICATION NUMBER: 10/465,789
PRIOR FILLING DATE: 2003-06-18
PRIOR FILLING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: 60/536,281
PRIOR FILLING DATE: 2004-01-13
PRIOR PELICATION NUMBER: 60/252,233
PRIOR PELICATION NUMBER: 60/252,233
PRIOR PILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 136
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SOFTWARE: Patentin version 3.1
SEQ ID NO 65
LENGTH: 66
TYPE: DNA
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LENGTH: 54
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No.
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                                                                                                        Query Match
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CURRENT APPLICATION NUMBER: US/11/033,489
CURRENT FILING DATE: 2005-01-11
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/465,789A CURRENT FILING DATE: 2003-06-18 PRIOR APPLICATION NUMBER: 09/990,087 PRIOR FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/252,233 PRIOR APPLICATION NUMBER: 60/252,233 PRIOR FILING DATE: 2000-11-20
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APPLICANT: Bayburt, Timothy
APPLICANT: Schuler, Mary A
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APPLICANT: Grimme, Stephen G.
TITLE OF INVENTION: Membrane Scaffold Proteins
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TITLE OF INVENTION: Membrane Scaffold Proteins
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                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                          Local Similarity
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                                 3 ATGGAATGATACCGTCA 19

Bayburt, Timothy H
Schuler, Mary A
Civjan, Natanya R
Yelena V. Grinkova

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Denisov, Ilia G.
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No. US20040053384A1
                                                                        Conservative
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                                                                                        69.0%;
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88.2%; Pred. No. 6.2e+03;
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                                                                                        Score 13.8; DB 7;
Pred. No. 6.4e+03;
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                                                                                                          Length 66;
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US-11-036-317-473162/c
                                                                                                                         ; ORGANISM: Mus musculus US-11-036-317-473162
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; ORGANISM: Mus musculus
US-10-719-900-744113
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US-10-719-900-744113/c
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 744113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 744113, Application US/10719900 Publication No. US20050026164A1 GENERAL INFORMATION:
                                                             Matches
                                                                                                                                                                                   SEQ ID NO 473162
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                          Sequence 473162, Application US/11036317
Publication No. US20050214823A1
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                                                                                          Query Match
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Best Local (
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Best Local Similarity
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                         APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                        TYPE: DNA
                                                                                                                                                                     ENGTH: 25
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25
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TTTGGAATGACACCGTC
                           TATGGAATGATACCGTC 18
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                                                           Conservative
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88.2%;
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88.2%;
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88.2%;
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Pred. No. 5.6e+03;
0; Mismatches 2
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                                                                        Score 13.8; DB 10 Pred. No. 5.6e+03;
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Pred. No. 5.6e+03;
                                                           Mismatches
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APPLICANT: DAUTRY-VARSAT, ALICE
ITITLE OF INVENTION: SECRETED CHLAMYDIA POLYPEPTIDES, POI
ITITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USES THE
FILE REFERENCE: 249179US0
CURRENT APPLICATION NUMBER: US/10/784,880
CURRENT FILING DATE: 2004-02-24
FRIOR APPLICATION NUMBER: US 60/448,879
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 378
SOFTWARE: Patentin version 3.1
SEQ ID NO 328
LENGTH: 30
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                                                       US-10-465-789A-32
                                                                            RESULT 20
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US-10-784-880-328
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                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic DNA US-10-784-880-328
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; ORGANISM: Mus musculus
US-11-036-317-985351
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Sequence 32, Application US/10465789A Publication No. US20040053384A1 GENERAL INFORMATION:
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SOFTWARE: Microarray Probe Sequence Listing Generator SEQ ID NO 985351
                                                                                                                                                                                                         Matches
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Best Local Similarity
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Publication No. US20050214823A1
GENERAL INFORMATION:
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILLING DATE: 2005-01-13
CURRENT FILLING DATE: 2005-01-6
PRIOR APPLICATION NUMBER: US 60/536,639
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                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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88.2%;
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88.2%;
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Pred. No. 5.7e+03;
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Pred. No. 5
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APPLICANT: Sligar, Stephen G APPLICANT: Bayburt, Timothy H APPLICANT: Schuler, Mary A

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Sequence 494473, Application US/11036317

Publication No. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR PILING DATE: 2004-01-13

NUMBER OF SEG ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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US-10-719-900-612502/c
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; ORGANISM: Rattus norvegicus
US-10-719-956-72805
                                                                                                                                                                                ; ORGANISM: Mus musculus 
US-11-036-317-494473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 612502, Application US/10719900 Publication No. US20050026164A1
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Best Local Similarity 93.8%;
Matches 15; Conservative
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                                                                                                                      Query Match 71.0%;
Best Local Similarity 84.2%;
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APPLICANT: Xue Mei Zhou

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT APPLICATION NUMBER: US/10/719,900

CURRENT FILING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002 11 20

NUMBER OF SEQ ID NOS: 982914

NUMBER OF SEQ ID NOS: 982914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                                                                                                                                                      TYPE: DNA
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Local Similarity 93.8%;
nes 15; Conservative
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                                                        TTATGGAATGATACCGTCA 19
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Pred. No. 2.7e
0; Mismatches
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Pred. No. 2.7e+03;
                                                                                                      Score 14.2; DB 10
Pred. No. 3.5e+03;
0; Mismatches 3
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RESULT 13
US-10-719-956-313188/c
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; ORGANISM: Rattus norvegicus
US-10-719-956-313188
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Sequence 275339, Application US/10719900
Publication No. US20050026164A1
GENERAL INFORMATION:
APPLICAMT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3528.1
CURRENT APPLICATION MYDER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
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NUMBER OF SEQ ID NOS: 699466
SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 313188
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Matches
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SOFTWARE: Microarray Probe (
SEQ ID NO 263303
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APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
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APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3527.1
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Best Local Similarity
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
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CURRENT FILLING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILLING DATE: 2002 11 20
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                  Score 13.8; DB 8; Length 25; Pred. No. 5.6e+03;
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Pred. No. 5.6e+03
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                                                            of Mouse
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PRIOR APPLICATION NUMBER: 60/427,808 PRIOR FILING DATE: 2002 11 20 NUMBER OF SEQ ID NOS: 982914

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                                                                                                                             US-10-745-242A-31
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Publication No. US200
GENERAL INFORMATION:
                                                                                                                                                                           SEQ ID NO 31
LENGTH: 20
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CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 34
                                                               Matches
                                                                                              Query Match
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                                                                                                                                                                                                      APPLICANT: Johnson, Jason M
TITLE OF INVENTION: Alternatively Spliced Isoforms of Histone Deacetylase 3 (HDAC3)
FILE REFERENCE: RS0207Y
CURRENT APPLICATION NUMBER: US/10/745,242A
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US 60/437,666
PRIOR EILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 60/478,233
PRIOR PLIING DATE: 2003-06-12
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.2
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APPLICANT: Loerch, Patrick
APPLICANT: Castle, John C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
FILE REFERENCE: PTS-0022
                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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TYPE: DNA
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Castle, John C
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No. US20040077578A1
                                                              Conservative
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85.0%;
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100.0%; Pred. No. 12
tive 0; Mismatches
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Pred. No. 16
                                                                           1e+03;
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RESULT 10
US-10-719-956-72805
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; ORGANISM: Probe Sequence
US-10-956-157-296567
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 296567
LENGTH: 25
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APPLICANT: Mounts, William
APPLICANT: Mounts, William
APPLICANT: MOUNTS, WILLIAM
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 296568
LENGTH: 25
SEQ ID NO 296568
                                                                                                                                                                    Sequence 72805, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
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               APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
PRIOR FILING DATE: 2002 11 20
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TYPE: DNA
NUMBER OF SEQ ID NOS: 699466
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Pred. No. 1.1e+03;
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Pred. No. 1.
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RESULT 1
US-10-173-192-33
US-10-173-192-33
; Sequence 33, Application US/10173192
; Publication No. US20030236204A1
                        RESULT 3
US-10-633-528-33
; Sequence 33, Application US/10653528
; Publication No. US20040077578A1
; GENERAL INFORMATION:
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US-10-173-192-61/c
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Best Local S
Matches 20
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SEQ ID NO 61
LENGTH: 20
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APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dol
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Best Local
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APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
FILE REFERENCE: PTS-0022
CURRENT APPLICATION NUMBER: US/10/173,192
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2
FILE REFERENCE: PTS-0022
CURRENT APPLICATION NUMBER: US/10/173,192
CURRENT FILING DATE: 2002-06-14
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100
 APPLICANT: Brett P. APPLICANT: Kenneth
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LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                              TYPE: DNA
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Brett P. Monia
Kenneth W. Dobie
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US-11-060-756-54930
US-11-060-756-54942
US-11-060-756-54943
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Pred. No. 3.5;
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Sequence 54930, 1
Sequence 54942, 1
Sequence 54943, 1
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RESULT 4
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CURRENT APPLICATION NUMBER: US/10/653,528
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 33
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                            Sequence 34, Application US/10173192
Publication No. US20030236204A1
GENERAL INFORMATION:
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LENGTH: 20
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Best Local Similarity
Matches 20; Conserv
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Best Local Similarity
                                                NUMBER OF SEQ ID NOS:
SEQ ID NO 34
LENGTH: 20
TYPE: DNA
                                                                            APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
FILE REFERENCE: PTS-0022
CURRENT APPLICATION NUMBER: US/10/173,192
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: PTS-0022
CURRENT APPLICATION NUMBER: US/10/653,528
CURRENT FILING DATE: 2003-09-02
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PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
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ORGANISM: H.
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                                 ORGANISM: Artificial Sequence
OTHER INFORMATION: Antisense Oligonucleotide
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                                       Published_Applications_NA_Main:*

1: /cgm2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgm2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgm2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

4: /cgm2 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

5: /cgm2 6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

6: /cgm2 6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

7: /cgm2 6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

8: /cgm2 6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgm2 6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgm2 6/ptodata/1/pubpna/US11E_PUBCOMB.seq:*
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US-10-719-906-15290

US-11-036-317-494473

US-10-719-900-275303

US-10-719-900-275303

US-10-719-900-275303

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US-11-036-317-491162

US-11-036-317-985351

US-10-7465-789A-32

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US-11-033-489-32

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US-10-719-956-222031
US-10-719-956-326638
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Sequence 655, App Sequence 4375, App Sequence 3115, App Sequence 3115, App Sequence 17126, App Sequence 21224, A Sequence 21224, A Sequence 49581, A Sequence 49581, A Sequence 49586, A Sequence 103924, Sequence 103924, Sequence 103924, Sequence 103225, Sequence 628624, Sequence 628624, Sequence 104445, Sequence 535142, Sequence 75543, A Sequence 75543, A Sequence 75543, A Sequence 95070, Asequence 86072, A
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Sequence 114407,
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Sequence 52437, A
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RESULT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08614686A
Patent No. 5830692
GENERAL INFORMATION:
APPLICANT: B CK. Anomat.
                                                                                      APPLICATION UNMBER: US/08/614,686A
FILING DATE: MARCH 12, 1996
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: GR19510930
FILING DATE: 24 MARCH 1995
APPLICATION NUMBER: GR19514056.7
FILING DATE: 13 APRIL 1995
ATTORNEY/AGENT INFORMATION:
NAME: COllard, Allison C.
REGISTRATION NUMBER: 22,532
REFERENCE/DOCKET NUMBER: 22,532
REFERENCE/DOCKET NUMBER: BOCK ET AL.-
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: 26,048
REGISTRATION NUMBER: 26,048
REGISTRATION NUMBER: BOCK ET AL.-
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: BOCK ET AL.-
ATTORNEY/AGENT INFORMATION:
NAME: Freedman, Edward R.
REGISTRATION NUMBER: BOCK ET AL.-
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 765:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: ISM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect Version 5.1
CURRENT APPLICATION DATA:
NAME: Keusey, Edwin H.
REGISTRATION NUMBER: 34,361
REFERENCE, DOCKET NUMBER: BO)
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Roslyn
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 11576
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: oligonucleotide primer SEQUENCE DESCRIPTION: SEQ ID NO: 765:
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1077 No. 5830692thern Boulevard
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                          BOCK ET AL.-4
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US-08-614-686A-6
                                               Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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POSITION IN GENOME:
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                   1 TTATGGAATGATACCGT 17
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                                                                                                                                                                   genomic DNA
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                                                              Score 12.2; DB 2;
Pred. No. 5.9e+03;
                                                   Mismatches
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Search completed: March Job time: 63.3333 secs 2, 2006, 01:01:34

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                                                                                                     Patent No. 6352829
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08,
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvilli, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: oligonucleotide primer
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                         APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvilli, Ro
              NUMBER OF SEQUENCES:
                                         Bibilashvilli, Robert TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 base pairs
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                                                                                                                                     Application US/09225928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08859998
                                                                                                                                                                                                                                                                               Conservative
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82.4%;
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                           EXPRESSION
              1375
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Pred. No. 5.8e+03;
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                                                                                                                                                                                                                                                                                                          DB 2;
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US-09-25-201B-765
; Sequence 765, Application US/09225201B
; Patent No. 6489455
; Fatent No. 6489455
; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chenchik, Alex
Jokhadze, George
Bibilashvilli, R
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                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: Windows95
SOFTMARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: lin
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                                                                                                                                                                                                                         ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100 CITY: Menlo Park
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                                                                                                                                                                                                            STATE: CA
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               APPLICATION NUMBER: US/09/225,201B FILING DATE: 05-Jan-1999
                                                                                                                                                                      ZIP: 94025
                                                                                                                                                                                        COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson, P.C. STREET: 2200 Sand Hill Road, Suite 100 CITY: Menlo Park
STATE: CA
CLASSIFICATION: <Unknown>
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82.4%;
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Pred. No. 5.
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                                                                                                                                                                           RESULT 25
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; ORGANISM: Homo sapiens
US-09-526-193A-99
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                                                                                                                                                         US-09-916-510A-9
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PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR PRIOR DATE: 1999-06-07
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
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CURRENT APPLICATION NUMBER: US/09/696,791
CURRENT FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 4523
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3914
LENGTH: 19
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                  Sequence 9, Application US/09916510A
Patent No. 6544507
GENERAL INFORMATION:
APPLICANT: IGGO, RICHARD D.
APPLICANT: BRUNDRI, MICHELE A.
APPLICANT: INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
PILE REFERENCE: 604-596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hayden, Michael R.
APPLICANT: Brooks Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
TITLE OF INVENTION: CHOLESTEROL LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tritz, Richard
TITLE OF INVENTION: RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: S.I.A. AND EYE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/526,193A
CURRENT FILING DATE: 2000-03-15
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SOFTWARE: FastSEQ for Windows Version
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NUMBER: US/09/916,510A
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Pred. No. 5.6e.
O; Mismatches
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Pred. No. 5
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CURRENT FILING DATE: 2001-07-3
PRIOR APPLICATION NUMBER: GB 99
PRIOR FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 22
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US-08-902-585-4
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S
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                             Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/844
PILING DATE: 18-APR-1997
APPLICATION NUMBER: 960799
PILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORWATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,89
REFERENCE/DOCKET NUMBER: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Primer
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/902,585
FILING DATE: 29-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                          MOLECULE TYPE:
                                                                                                                                      LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                   TELEFAX: 610-270-5090
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Similarity 82.4%;
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TTATGGAATGATACCGT 17
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                                Conservative
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                                                                                                                            linear
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                                                                                                            Genomic DNA
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                                              61.0%;
82.4%;
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                                                                                                                                                                                                                                                                                               38,891
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                                              Score 12.2; DB 2;
Pred. No. 5.8e+03;
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Pred. No. 5.7e+03;
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                                 Mismatches
                                                               2
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; OTHER INFORMATION: Antisense Oligonucleotide US-09-705-299-38
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APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Bhallelic markers for use in
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER APPLICATION NUMBER: US 60/082,614
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US-09-422-978-1307
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; OTHER INFORMATION: Primer
US-09-488-265B-52
                                                                                                                                                                                                                                                                                                                                           US-09-705-299-38/c
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                                                                                                                                                                                                                        Sequence 38, Application US/09705299
Patent No. 6440737
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
Query Match
Best Local Similarity
                                                                                                                                      SEQ ID NO 38
LENGTH: 20
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LENGTH: 47
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Best Local Similarity
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                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/705,299
CURRENT FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 86
                                                                                               TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: allele
LOCATION: 24
                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 99-22712-242 : polymorphic base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foca
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                                                                                                Sequence
62.0%;
92.9%;
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Pred. No. 3.9e
0; Mismatches
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Pred. No. 3.7e+03
Score 12.4; DB 3;
Pred. No. 4.5e+03;
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; Sequence 3914, Application US/09696791 ; Patent No. 6770633 ; GENERAL INFORMATION:
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US-08-288-663A-4
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APPLICANT: ONDA, Haruo
TITLE OF INVENTION: HUMAN TRH R
TITLE OF INVENTION: AND USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: 09-AUG-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                          MOLECULE TYPE: Other nucleic acid, synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HINUMA, Shuji
APPLICANT: HOSOYA, Masaki
                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Resnick, David REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-AUG
APPLICATION NUMBER:
FILING DATE: 16-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-523-6440
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                                                                                                                                                                                                                                                                                                        LENGTH:
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92.9%;
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                                                                                                                                                                  Score 12.4; I
Pred. No. 4.8e
0; Mismatches
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APPLICANT:

Robbins,

Joan M.

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US-09-396-196G-10050/c
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOPTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 10050
             Sequence 28, Application US/09684855
Patent No. 6599735
GENERAL INFORMATION:
APPLICANT: F. Hoffmann-La Roche AG
TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
FILE REFERENCE: C18435/111692
CURRENT APPLICATION NUMBER: US/09/684,855
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Patent No. 6821724
GENERAL INFORMATION:
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Best Local :
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Matches 15; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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APPLICANT: David Mack
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 3730,204-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 25
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: DK 0420/92
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David Lockhart
                                                                                                                                                                                                                                                                                      Conservative
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78.9%;
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Pred. No. 3.6e+03
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                                                                                                                                                                                                                                                                                                                        DB 3;
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RESULT 18
US-09-684-855-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: F. HOÉFMANN-LA ROCHE AG
TITLE OF INVENTION: CONTINUOUS FERMENTATION PRO
FILE REFERENCE: C38435/111692
CURRENT APPLICATION NUMBER: US/09/684,855
CURRENT FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: EP 00121663.9
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 1999-10-11
NUMBER OF SEQ ID NOS: 169
                                                                                                                                                                                                                                             US-09-488-265B-52/c
                                                                                                                                                                                                                                                              RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6599735
GENERAL INFORMATION:
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                                                                                                                                                                                                         Sequence 52, Application US/09488265B Patent No. 6720174
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Best Local :
                  SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
LENGTH: 31
                                                                                                                                                                                          GENERAL INFORMATION:
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Best Local S
                                                                        APPLICANT: Lehmann, Martin
APPLICANT: Lassen, Soren F
TITLE OF INVENTION: Improved Phytases
FILE REFERENCE: 5808.200-US
CURRENT APPLICATION NUMBER: US/09/488,265B
CURRENT FILING DATE: 2000-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: EP 00121663.9 PRIOR FILING DATE: 2000-10-04 PRIOR FILING DATE: 2000-10-04 PRIOR APPLICATION NUMBER: EP 99120289.6 PRIOR FILING DATE: 1999-10-11
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                                                                    NUMBER OF SEQ ID NOS: 98
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LENGTH: 31
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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78.9%;
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Pred. No. 3.7e+03;
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Pred. No. 3.7e+03;
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ORGANISM: Artificial Sequence

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US-10-131-827-7377
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; ORGANISM: Homo sapiens
US-10-131-827-3115
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Matches
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7377
LENGTH: 50
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3115
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                                                  PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
                                                                                                                                          APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILLING DATE: 2002-09-06
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT EXPELICATION NUMBER: US/10/131,827
CURRENT FILLING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILLING DATE: 2001-10-20
PRIOR FILLING DATE: 2001-06-08
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ORGANISM: Mus musculus
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Woodward, Robert
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Pred. No. 1.8e+03;
0; Mismatches 3
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Pred. No. 1.9e+03
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US-09-396-196G-75543
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APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 75543
                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5,
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APPLICANT: Dorrei
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: mus musculus
                                       ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
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                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         APPLICANT: Mischler, Marcel
APPLICANT: Dalboge, Henrik
APPLICANT: Heldt Hansen, Hans P.
TITLE OF INVENTION: A NOVEL ENZYME AND A DNA SEQUENCE
                                                                                                                                                                               STREET: 405 Le
CITY: New York
STATE: New Yor
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CLASSIFICATION:
             APPLICATION NUMBER: US/08/313,050 FILING DATE: 05-OCT-1994
                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                             New York
                                                                                                                                                                                                            E: No. 55852560 No. 5585256disk of No. 5585256th America, Inc. 405 Lexington Avenue, 64th Floor
                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                               Dorreich, Kurt
Christensen, Fl
Schnell, Yvette
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87.5%;
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Pred. No. 1.9e+03;
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US-09-699-135-25
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US-09-463-702A-25
                                                                                                  RESULT 9
US-09-396-196G-15329/c
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                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: PRIMER 3' GSP2 US-09-699-135-25
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/699,135
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US/09/463,702A
; PRIOR FILING DATE: 2000-01-24
; PRIOR APPLICATION NUMBER: PCT/JP98/03114
; PRIOR APPLICATION NUMBER: PCT/JP98/03114
; PRIOR FILING DATE: 1998-07-10
; PRIOR FILING DATE: 1997-07-25
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Pa
SEQ ID NO 25
LENGTH: 24
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LENGTH: 24
                                              Sequence 15329, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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GENERAL INFORMATION:
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Best Local Similarity
APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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CURRENT FILING DATE: 2000-01-24
PRIOR APPLICATION NUMBER: DET/JP98/03114
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: JAPAN 9/200387
PRIOR FILING DATE: 1997-07-25
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: AGENE Research Institute, Co., APPLICANT: HIRAKI AND ASSOCIATES APPLICANT: SHIMAMOTO, AKIRO
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TYPE: DNA
ORGANISM: ARTIFICIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FURUICHI, YASUHIRO
TITLE OF INVENTION: HUMAN GENE RECQ4 ENCODING HELICASE
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                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09699135
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Pred. No. 1.7e+03;
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; ORGANISM: Mus musculus
US-09-396-196G-18885
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APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local S
Matches 15
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SEQ ID NO 18885
LENGTH: 25
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LENGTH: 25
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
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l Similarity 83.3%;
15; Conservative
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Pred. No. 1.8e+03;
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PRIOR APPLICATION DATA:

CLASSIFICATION:

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           Sequence 1662, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use
FILE REFERENCE: GENSET.020CP1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Timo KORPEIA et al.
TITLE OF INVENTION: Microbial protein expression system
FILE REFERENCE: 0933-0175P
CURRENT APPLICATION NUMBER: US/09/959,650
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 25
SOPTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/422,978
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 26
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
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FILING DATE: 29-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,4
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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84.2%;
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Pred. No. 5.3e+02;
0; Mismatches 3
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Pred. No. 5.4e+02;
0; Mismatches 3;
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                          in constructing a high density...
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-3668
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                                                                                                                                                                                           RESULT 7
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                                                        GENERAL INFORMATION:
APPLICANT: AGENE Research Institute,
APPLICANT: HIRAKI AND ASSOCIATES
APPLICANT: SHIMAMOTO, AKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 3668
                                                                                                                                  Sequence 25, Application US/09463702A Patent No. 6335435
                                                                                                                                                                                                                                                                                                                             Matches
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Best Local (
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Patent No. 6905827
GENERAL INFORMATION:
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SEQ ID NO 1662
LENGTH: 47
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   APPLICANT: KITAO, SAORI
APPLICANT: FURUICHI, YA
TITLE OF INVENTION: HU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Woodward, Robert
APPLICANT: LY, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMU
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robes
APPLICANT: Ly, Ngoc
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EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 10/006,290 PRIOR FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo Sapiens
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Local Similarity 80.0%;
les 16; Conservation
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Pred. No. 1.2e.
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US-08-592-936B-7/c
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           Sequence 18, Application US/08788928A
Patent No. 5783394
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bestwick, Richard K.
APPLICANT: Kellogg, Jill A.
TITLE OF INVENTION: RASSBERRY PRON
TITLE OF INVENTION: TRANSGENES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5783393
GENERAL INFORMATION:
APPLICANT: Kellogg, Jill A.
APPLICANT: Bestwick, Richar
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
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TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR
TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DruGen 3' primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: EVAND, SUBAN T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 42:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,936B
FILING DATE: 29-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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5. 5783393
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SEQUENCES:
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350 Cambridge Avenue, Suite 250
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RASPBERRY PROMOTERS FOR EXPRESSION OF TRANSGENES IN PLANTS
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84.2%; Pred. No. 5.3e+02;
rive 0; Mismatches 3;
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US-08-469-419-38
US-08-934-386-42
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Sequence 38,
Sequence 42,
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Sequence 7, Application US/091115
Patent No. 5929302
GENERAL INFORMATION:
APPLICANT: Kellogg, Jill A.
APPLICANT: BESTWICK, RICHARD
TITLE OF INVENTION: PLANT TIS
TITLE OF INVENTION: REGULATED
NUMBER OF SEQUENCES: 27
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/
PILING DATE: 29-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: EVANB, SUSAN T.
REGISTRATION NUMBER: 38,44
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LEW PC compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
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ANTI-SENSE: 1
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION INMEER: US/08/788,928A FILING DATE: 24-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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ADDRESSEE: Dehlinger & Associates
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ADDRESSEE: Dehlinger & Associates
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CITY: Palo Alto
STATE: CA
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TOPOLOGY: linear
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                                                                                                                    ZIP: 94306
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84.2%;
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PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR REGULATED EXPRESSION OF TRANSGENES IN PLANTS
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Pred. No. 5.3e+02;
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/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PE_COMB.seq:*
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9-488-2658-52
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Sequence 765, App
Sequence 15, Appli
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Sequence 14, Appli
Sequence 90391, A
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Sequence 100, Appli
Sequence 10, Appli
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Sequence 2, Appli
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Sequence 105, Appli
Sequence 15, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
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                                                                                                                                                                                                                    AL952980 42 bp I
Arabidopsis thaliana T-DNA flanking
genomic survey sequence.
AL952980
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Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database
                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                            SSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 pp DNA linear GSS SALK 072158.26.45.x Arabidopsis thaliana TDNA insertion Arabidopsis thaliana genomic clone SALK_072158.26.45.x, survey secuence.
                                                                                                                                                                                              AL952980.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
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Arabidopsis thaliana
                                                                                                                                                 Arabidopsis thaliana (thale cress)
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                  eurosids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="SALK_072158.26.45.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                GI:24409602
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82.4%;
                                                             Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 1.4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone MVA11. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the Graman Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (bases 1 to 42)
Rosso, M.G., Li, Y.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutagenized Arabidopsis thaliana
BioTechniques 35 (6), 1164-1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the identification of T-DNA insertion mutants in Arabidopsis thaliana
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                                                                                                                  Similarity
ATGGAAGTATACCGCCA 31
                                           ATGGAATGATACCGTCA 19
                                                                                            Conservative
                                                                                                                                                                                                          fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed "
                                                                                                                                                                                                                                                                           /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAc161 (denBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana'
/mol_type="genomic DNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                                                        clone="GK-347E08-016235"
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                                                                                            <u>.</u>
                                                                                                             Score 12.2; DB 10
Pred. No. 1.4e+05;
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CW233625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CW233625 78 bp DNA linear GSS 30-OCT-2004 104 687_11213545_116_37381_015 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11213545, genomic survey
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                                                                                                                                                                                                                                                                                                  Orion Genomics, LLC
4041 Forest Park Ave,
Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sorghum bicolor
                                                                                                                                                                                                                 Email: jbedell@oriongenomics.com plate: 687 row: b column: 01 Seq primer: T3 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sorghum genome sequencing by methylation filtration PLoS Biol. 3 (1), e13 (2005)
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//clone lib="Sorghim bicolor SLCot"
//clone lib="Sorghim bicolor SLCot"
//clone weteror: pGEM-TA-Easy; A Cot analysis was performed for the sorghim genome. Based on the resulting Cot curve, hydroxyapatite chromatography was used to isolate 'highly-repetitive' (FR), 'moderately-repetitive' (FR), and 'single/low-copy' (SL) sequence components from sheared genomic DNA. The three repetition-based DNA components were cloned into E. coli to produce HRCot, MRCot, and SLCot genomic libraries. Blotting and sequencing data indicates that each library is representative of the component from which it was derived. Putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI Nr Database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot clone' contain the complete sequence of its putative Nr match."
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cultivar="BTx623"
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/mol_type="genomic DNA"
/cultivar="ATx623"
/db_xref="taxon:4558"
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                                                                                 /organism="Sorghum bicolor"
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CL528379/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.

1 (bases 1 to 80)

Mitchell, R.S., Beltzel, B.F., Schroder, A.R.W., Shinn, P., Chen, H., Berry, C.C., Ecker, J.R. and Bushman, F.

Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Targe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TGGAATGATACCGT 17
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ASV12E06.fwd ASLV-vector integration sites in human 293T-TVA cells
Homo sapiens genomic clone ASV12E06.fwd, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: PCR with specific primers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 858 453 4100 x1630 Fax: 858 554 0341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site Preferences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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TATGGAATGATACC 15
                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bushman@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated too enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                              /note="Human 293T cells expressing the subgroup A avain retrovirus receptor (293T-TVA) were infected with an ASIV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the ASIV cDNA. Junctions between integrated ASIV proviruses and cellular DNA were cloned and sequenced."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293T-TVA cells"
                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                         clone_lib="ASLV-vector integration sites in human
                                                                                                                                                                                                                                                                                                                                                               clone="ASV12E06.fwd"
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92.9%;
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92.9%;
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Pred. No. 1.2e+05;
                                             Score 12.4; DB 10;
Pred. No. 1.2e+05;
0; Mismatches 1;
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CL656659
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AZ922984/c
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                                                                                          Peterson, D.G., Schulze, S.R., Sciara, E.B., Lee, S.A., Bowers, J.E., Nagel, A., Jiang, N., Tibbitts, D.C., Wessler, S.R. and Paterson, A.H. Integration of Cot analysis, DNA cloning, and high-throughput sequencing facilitates genome characterization and gene discovery
                                                                                                                                                                                                                                                                  Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CL656659 70 bp DNA linear GSS 09-JUL-2004 PRI0127a_H08 - PRI0127a_B21 (70) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
University of Georgia
               Plant Genome Mapping Laboratory
                                      Contact: Peterson DG
                                                                               Genome Res. 12 (5), 795-807
                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Srinivasan, J., Otto, G.W., AppaDB: an AcedB database
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
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/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of
var. California"
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Pred. No. 1.1e+05;
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                                                                               (2002)
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                                      Email: dgp@arches.uga.edu
Class: Hydroxyapatite-fractionated
                                                                                                                                                                             Plant Genome Mapping Laboratory
University of Georgia
                                                                                                                                                                                                                             Contact: Peterson DG
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
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Sorghum bicolor
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AZ922992
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Fax: 706-583-0160
                                                                                                                                                            Room 162
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Class: Hydroxyapatite-fractionated
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/clone lib="Sorghum bicolor SLCct"
/note=Tvector: pGEM-TA-Easy; A Cot analysis was performed
/note=Tvector: pGEM-TA-Easy; A Cot analysis was performed
for the sorghum genome. Based on the resulting Cot curve,
hydroxyapatite chromatography was used to isolate
'highly-repetitive' (HR), 'moderately-repetitive' (MR),
and 'single/low-copy' (SL) sequence components from
sheared genomic DNA. The three repetition-based DNA
components were cloned into E. coli to produce HRCot,
MRCot, and SLCot genomic libraries. Blotting and
sequencing data indicates that each library is
representative of the component from which it was derived.
Putative ID listings given for sequences are based on
comparison (blastn) with sequences in the NCBI Nr
Database. Only the primary match is given (all primary E
values are < or = 1.00E-5). In no instance does a 'Cot
clone' contain the complete sequence of its putative Nr
match."
                                                                                                                                         USA
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/mol_type="genomic
/cultivar="BTx623"
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                                                                                                                                                       Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.4; DB 9;
Pred. No. 1.1e+05;
0; Mismatches 1
                                           DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA.
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CO745042/c
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AUTHORS
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 bp mRNA linear EST 30-JUI
TgESTzyp25g10.y2 Tg CAST Tachyzoite cDNA Library 2 Toxoplasma
gondii cDNA clone TgESTzyp25g10.y2 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                         Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Sowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareisbvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.

Toxoplasma EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxoplasma gondii
Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope
                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Clifton, S.
                                                                                                                                                                                                                                   information relating to organism, Putative full length read vector to vector length is Seq primer: T7 from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sarcocystidae; Toxoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO745042.1 GI:50858573
                                                                                                                                                                                                                                                                                                                          Contact David Sibley
                                                                                                                                                                                                                                                                                                                                               Email: toxo@watson.wustl.edu
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                                                            /organism="Toxoplasma gondii"
/mol type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTzyp25g10.y2"
/dev_stage="Tachyzoite"
/lab_host="GC10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="G"
/note="Genoscope sequence ID : C0BG012CC11LP1
end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/db xref="taxon:99883"
/clone="012F21"
/clone lib="Tg CAST Tachyzoite cDNA Library 2"
/note="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI;
cDNA library was constructed by Keliang Tang, and Rob
                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 8.7e+04;
                                                                                                                                                                                                                                                                                                                          (toxoest@borcim.wustl.edu) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                      libraries, or clone availability.
                                                                                                                                                                                                                                                                                                                                                                                                             St. Louis,
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RESULT 23
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Matches 15
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E 1 (bases 1 to 74)

S ambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Finch,R.A., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Key,B.W., Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.

Zhu,Q., Person,C. and Sands,A.T.

What kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention thereof the state of the s
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OST109611 Mus musculus 129Sv/Ev Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11) Class: Gene Trap.
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CG529309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Omni Bank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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                                                                                                                        Similarity
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TTATGGAATGATACCGTCA 19
                                                                                Conservative
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                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST109611"
/cell_type="embryonic ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cole at Washington University. Total RNA was converted to CDNA using the template-switching PCR method (Creator SMART cDNA, Clontech Inc.). First strand was PCR amplified using the same primer set and the fragments were digested with Sfil. The fragments were size selected, ligated into vector pDNR LIB containing directional Sfil sites, and electroporated into GC10 competent cells. WARNING: the library contains a small percentage of cDNAs derived from the human host cells."
                                                                                                                                                                                                                                                                    /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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                                                                                                                    63.0%;
                                                                        ; Score 12.6; D
; Pred. No. 8.9e
0; Mismatches
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Pred. No. 8.8e+04;
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                                                                                                                8.9e+04;
                                                                                                                                                            DB 10;
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REFERENCE AUTHORS

COMMENT

JOURNAL PUBMED TITLE

FEATURES

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TAATGGTCTCATACCGTCA 3

ORIGIN

VERSION KEYWORDS

DEFINITION ACCESSION

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ş 밁

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AUTHORS
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AJ587959/c
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Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Lepiniec, L., Caboche, M. and Lecharny, A.
                                                                                                                                           GSS; left border; T-DNA flanking sequence
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                            AJ587959 58 bp I
Arabidopsis thaliana T-DNA flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At5965020. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                    Spermatophyta; Magnoliophyta;
                                                                                                                     Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                         AJ587959.1 GI:37937583
                                                                                                                                                                                                                                                345C03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (bases 1 to 52)
Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flanking sequence tag-based reverse genetics plant Mol. Biol. 53 (1-2), 247-259 (2003)
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Bioinformatics 19 (11), 1441-1442 (2003)
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                                                                                  rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                              genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (denBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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ecotype="Col-0"
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78.9%;
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Pred. No. 8.6e+04;
                                                                                                    eudicotyledons;
                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                sequence,
                        Aubourg,S., Samson,F.
Rose,R., Pelletier,G.,
                                                                                                                     Embryophyta; Tracheophyta;
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                                                                                                    core eudicotyledons;
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left border, clone
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CNS03BOT/c
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plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsqap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL236774.1 GI:7895909
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Tetracdon nigroviridis genome survey sequence T7

012F21 of library G from Tetracdon nigroviridis,
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                                                                                                                                                                                                                                                        Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from
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|mol_type="genomic DNA"
|db_xref="taxon:3702"
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/ecotype="Wassilewskija"
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Pred. No. 8
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end of clone
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                                                                                                                                                                                                                                                                                                                   Campus, Hinxton, Cambridgeshire, CB10 1SA, U
humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end
is part of the Daniokey BAC Library created
                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-JAN-2003) The Sanger Institute, W Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (Dases 1 to 44)
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BX193212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Satoh,N., Satou,Y., Kohara,Y. and Shir
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                        Humphray, S.J., Huckle, E. and Durham, J.L.
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                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Keygene. Further details:
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                                                                                  Similarity
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                                 TTATGGAATGATACCGTCA 19
 TTATTGAATGATGCAGTAA 21
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db xref="taxon:7719"
/db xref="taxon:7719"
/clone="cleg24k14"
/clssue type="whole animal"
/tlssue type="whole animal"
                                                                                                                                               /clone="DKEY-204N22"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="Nori Satoh unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Ciona intestinalis"
                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                   organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%;
75.0%;
                                                                                63.0%;
78.9%;
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Pred. No. 8.
                                                                                Score 12.6; DB 10
Pred. No. 8.4e+04;
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                                                                                                                                                                                                                                                                                                                   from the SP6 end of BAC 204N22. 204N22 Library created by R. Plasterk and N.V.
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                                                                                                 DB 10;
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                                                                                                Length 44;
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. E-mail enquir:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            survey sequence
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JOURNAL COMMENT
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BZ289135/c
LOCUS
                        REFERENCE
AUTHORS
TITLE
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DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons;
core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                        AL759243 52 bp I
Arabidopsis thaliana T-DNA flanking
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BZ289135
Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database the identification of T-DNA insertion mutants in Arabidopsis
                                                                                                                                                                                                                GSS
                                                                                                                                                                                                                                                                                     genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="SALK_022532.47.40.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis
/mol_type="genomic DNA'
/ecotype="Col-0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%;
78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.6; DB 9;
Pred. No. 8.6e+04;
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                                                                                                                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                             sequence GK-166H08-013361,
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RESULT 14
CG515614/c
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PUBMED
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         Piggott, J., Beltrandelkio, H., Button, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B. W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Shu, Q., Person, C. and Sands, A.T.
Wukl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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OST71843 Mus musculus 129Sv/Ev N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ហ
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'http://genetrap.gsf.de/project/web new/database/result_clone.html?
clone_id=A035B06' ES cell line harboring insertion mutation of
target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm
                                                                                                                                                                                                                                      Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                                                                          Email: materials@lexgen.com
                                                                                                                                                                                                                                                                                                         Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 77)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                    Contact: Zambrowicz BP
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                                                                                                                                                                                                                       Gene Trap
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 1298v/Ev"
                                               /db_xref="taxon:10090"
/clone="OST71843"
                                                                                              /mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/note="Vector: pTlbetageo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:10090"
'clone="A036B06"
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strain="129 Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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87.5%;
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Pred. No. 7e+04;
0; Mismatches
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SOURCE
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AV963579
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                                                                                                                                                                                                                                                          15
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Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venylary J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                     AV963579 Nori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg24k14 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                       2 TATGGAATGATACCGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ark/Projects/T_brucei/.
                                                                                    AV963579.1 GI:19451878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL466263.1 GI:11835618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence
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Similarity 82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:5691"
/clone="137c05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA'
/strain="TREU927"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Trypanosoma brucei"
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                                                                                                                                                                                                                                                                                                                                               63.0%;
78.9%;
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                                                                                                                                                                                                                                                                                                                                             Score 12.6; DB 11
Pred. No. 8.3e+04;
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VERSION
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Best Local Similarity
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                      Chonju, 561-756, S. Korea Tel: +82-652-70-3340
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Emericella.

1 (bases 1 to 57)

Lee,D., Lee,S., Hwang,H., Kim,J. and Chae,K.

Quantitative analysis of gene expression in sexual structures of Aspergillus nidulans by sequencing of 3'-directed cDNA clones FEMS Microbiol. Lett. 138 (1), 71-76 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emericella nidulans (anamorph: Aspergillus nidulans)
Emericella nidulans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U44189 57 bp mRNA linear EST 03-APR-1996 ENU44189 Aspergillus nidulans cleistothecium Emericella nidulans CLONA clone SE0326, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TGGAATGATACCGTCA 19
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U44189
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Keon-Sang Chae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U44189.1 GI:1244852
                                                                                                                                                                                                                                                                              Email: chaeks@chonbuknms.chonbuk.ac.kr.
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Fax: +82-652-70-3345
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:162425"
/clone="SE0326"
/tissue_type="cleistothecium"
/cell_type="Hull cell"
/cell_type="Hull cell"
                                                                                                                                                                                                         /mol_type="mRNA"
/strain="FGSC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult, 17 years"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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|mol_type="mRNA"
                                                                                       /clone lib="Aspergillus nidulans cleistothecium"
/note="3′-directed cDNA clones; single-pass sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="Barstead spleen HPLRB2"
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                                                                                                                    dev_stage="sexual"
                                                                                                                                                                                                                                            organism="Emericella nidulans"
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87.5%;
              64.0%;
87.5%;
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<u>,</u>
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Pred. No. 6.7e+04;
D; Mismatches 2
                Score 12.8; DB 8; Pred. No. 6.8e+04;
 Mismatches
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                                                                                     single-pass sequencing"
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                                  Length 57;
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CL214052/c
LOCUS
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DEFINITION
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AV854960/c
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AV854960 Nori Satoh unpublished cDNA library, young adult Ciona
intestinalis cDNA clone rciad19kl2 3', mRNA sequence.
                                                                   1 (bases 1 to 76)
Hansen, J., Floss, T., van Sloun, P., Fuchtbauer, E.M., Vauti, F., Arnold, H.H., Schnutgen, F., Wurst, W., Von Melchner, H. and Ruiz A large-scale, gene-driven mutagenesis approach for the funct analysis of the mouse genome
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
                                                                                                                                                                                                                                                                                                A036B06 GGTC Gene Trap Library GV03C04 Mus A036B06, mRNA sequence. CL214052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 GGAATGATACCGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T. Expressed genes in Ciona intestinalis Unpublished (2000)
                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciona intestinalis
                                                                                                                                                                          Mammalia; Eutheria; Euarchontoglires; Glires;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                     CL214052
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                                      Contact: GGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 Genetrap Consortium (GGTC) info@genetrap.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="rciad19k12"
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                                                                                                                                                                                                                                                                                                                                                     76 bp
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                                                                                                                                                                                                                                                                                                                                                       mRNA
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Length 74;

Indels

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Gaps

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Linear GSS 22-MAR-2005 musculus cDNA clone

for the functional

and Ruiz, P.

Euteleostomi;

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BX892081/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana T-DNA genomic survey sequence. BX892081
                                                                         An Arabidopsis thaliana T-DNA mutagenized population flanking sequence tag-based reverse genetics plant Mol. Biol. 53 (1-2), 247-259 (2003)
                                                                                                                                                                                                                                                      Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis
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Strizhov, N., Weisshaar, B.
                                                                                                                                     Weisshaar,
                                                                                                                                                        Rosso, M.G., Li, Y.,
                                                                                                                                                                                                                   Bioinformatics 19 (11), 1441-1442 (2003)
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: methylation filtered
High quality sequence stop: 77.
Location/Qualifiers
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Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fsbb001f064 row: h colum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., McMenamy, J., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                          rosids; eurosids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martienssen, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4558"
/clone="fsbb001f064h09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cultivar="ATx623"
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                  Li,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.0%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                      II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                      Strizhov, N., Reiss, B.,
                Rosso, M.G.,
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Pred. No. 4.3e+04;
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                  Viehoever, P.,
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                  Dekker, K.A.
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                                                                                                                                                                                                                              1 (bases 1 to 49)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA985054 49 bp mRNA linear EST 27-MAY-1 am69f06.s1 Barstead spleen HPLRB2 Homo sapiens cDNA clone IMAGE:1577315 3' similar to SW:ATPO_BOVIN P13620 ATP SYNTHASE D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                               Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone MNA5. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                      Email: est@watson.wustl.edu
                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High-throughput generation of sequence indexes mutagenized Arabidopsis thaliana lines BioTechniques 35 (6), 1164-1168 (2003)
                                                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Direct Submission
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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ecotype="Col-0"
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Pred. No. 4.3e+04;
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eg 10, Koeln, 50829, Germany
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 65)
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CN924691 65 bp mRNA linear F 000415AELA008223HT (AELA) Royal Gala young expanding domestica cDNA clone AELA008223, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
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CN924691.1 GI:48397504
EST.
                                                                                                                                                       CZ486525
f03919-5prime Exelixis piggyBac WH insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of piggyBac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Facility
The Horticulture an
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                       2 TATGGAATGATACCGTCA 19
                                                                                                                                genomic survey sequence. CZ486525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Leaf"
/dev stage="Young, expanding"
/clome_lib="(AELA) Royal Gala young expanding leaf"
/clome_tib="(AELA) Royal Gala young expanding leaf"
/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AELA008223"
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83.3%;
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Pred. No. 4.1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 7;
Pred. No. 4.2e+04;
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                           Muscomorpha;
                                        Pterygota;
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AUTHORS
                                                                                                                                ORGANISM
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Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Sringh,C.M., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W., Rymer,L., Cheung,L.M., Chong,A., Brickson,C., Fisher,W.W., Rymer,L., Jack,L., Joo,D., Killpack,K., Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Woo,A., Zakrajsek,L., Zhao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J. Swimmer, C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J. A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, E
Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32
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Class: transposon insertion site.
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                      Sorghum bicolor (sorghum)
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Sorghum.

1 (bases 1 to 77)
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                                                                                                                                                                                                                                                                                          CW382475 77 bp DNA linear GSS 01-NC fsbb001f064h09f0 Sorghum methylation filtered library (LibID: Sorghum bicolor genomic clone fsbb001f064h09, genomic survey
                                                                                                                                                                                        GSS.
                                                                                                                                                                                                                                           sequence.
CW382475
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Genet. 36 (3), 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="Exelixis piggyBac WH insertions"
/clone="Vector: piggyBac WH (GenBank accession number AY515148); An isogenic w- Drosophila melanogaster strain x87515148); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. We remobilized the WH element using the constitutive alpha-1 tubulin:piggyBac transposase source. We remobilized the WH element from a single ammunition element on the Binsinscy balancer chromosome in dysgenic females. We outcrossed dysgenic virgin females in vials to the isogenic w- strain and selected new hops in the following generation. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."
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/mol type="genomic DNA"
/strāin="isogenic w- strain"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                       GI:55100919
Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
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Pred. No. 4.3e+04;
0; Mismatches 3;
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TY (LibID: 104)
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Best Local
Matches :
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                                                                                                                                                                                                                                                                                                                                           to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                                                                                                                                                                                                               Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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T. brucei sheared genomic DNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
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AL495665
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                                                                                                                                                                                                                                                                                                                              Oxford
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="374d04"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                           organism="Trypanosoma brucei"
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/).
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                                                                                                                                                                                                                                                                                                                          University Press, 1999).
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Pred. No. 2.6e+04;
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RESULT 4 TA374D04P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Fax: 801 585 7177
Insert Length: 10000 Std Error: C
Plate: 0053 row: H column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2M0053H15R Mouse 10kb plasmid UUGC1M library Muclone UUGC2M0053H15 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 48.
                                                                Conservative
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                        /note=^{\rm T}Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant,
/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
                                                                                                                                                                                                                                                                                                                                                                                     /sex≂"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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Pred. No. 2.6e+04;
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                                                                                                                                                                                                                                                                                                        Jackson
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CG530112/c
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BW510050
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Whkl kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG530112 73 bp
OST111465 Mus musculus 129Sv/Ev
mRNA sequence.
CG530112
CG530112.1 GI:37316684
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Ciona savignyi
Ciona savignyi
                                                                                 BW510050 Yutaka Satou beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Zambrowicz BP
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                                         BW510050.1 GI:51671748
                                                        library Ciona savignyi
BW510050
                                                                                                                                                                                                                                                                                                                                                                                                                                     described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4000 Research Forest Drive, The Woodlands, TX 77381, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lexicon Genetics Incorporated
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                     TTATTGAATGATACAGTNAT 24
                                                                                                                                                                                   TTATGGAATGATACCGTCAT 20
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588 588
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                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="129Sv/Ev"
                                                                                                                                                                                                                                                                                                                        /clone="OST111465"
                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence tag generated by 3' in Zambrowicz et al (Nature.
                                                                                                                                                                                                                                                                                              clone
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                                                                                                                                                                                                                                                                                             _type="embryonic stem cell"
e_lib="Mus musculus 129Sv/Ev"
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AG206339
AG189033
CR357573
                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                       Score 15.8; DB 10
Pred. No. 1.7e+03;
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                                                                      cDNA clone
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                                                                     n downstream gene csbt001d09, mRNA
                                                                                                                                                                                                                                                    DB 10;
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                                                                                                  TIRINA
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1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                                    Length
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AG189033 Pan trogl
CR357573 Arabidops
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OST111465,
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42 TTATGGNATTATAACGNNAT 61
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1 (bases 1 to 79)
Imai, K.S., Satoh, N. and Satou, Y.
Expressed genes in Ciona savignyi (Imai, Satoh, Satou)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 bp DNA linear GSS 04-OCT-200
1M0290M14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0290M14 F, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTATGGAATGATACCGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R. Mouse whole genome scaffolding with paired end reads from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yutaka Satou
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                             Sequence
                                                                                                                                                                               atherosclerosis, congrete rheumatoid arthritis,
                                                                                                                                                                                                rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus crythem
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08-JUN-2001; 2001US-0296764P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte gene expression profiling
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 TATGGAATGAGACCACCA
                                   TATGGAATGATACCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     for leukocyte expression profiling, diagnosing a disease, or (the rate of) progression of a disease, e.g. atherosclerosis ive heart failure, comprises diagnostic oligonucleotides.
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                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     565; Opp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2003;
25-NOV-2003;
25-NOV-2003;
The invention relates to a novel method for identifying a subject of breast cancer comprising detecting the presence or absence of polymorphic variation associated with breast cancer. The method of invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer metastasis. The methods may be utilized for gene therapy of the cancer metastasis. The methods may be that of a PCR primer of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADX98978
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                                                                                                                                                                                                                                                                                                               Identifying risk of, preventing and/or treating breast cancer by identifying and/or analyzing polymorphic variations in nucleotide sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoyal-Wrightson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roth RB,
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ghtson CR;
                                                                                                                                                                                                                                                       Page 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast tumor; endocrine disease; obstetrics; neoplasm; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 A;
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Query Match Best Local Similarity

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RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention which was used to amplify a human intercellular adhesion molecule (ICAM1, ICAM4, ICAM5) region DNA containing a single nucleotide polymorphism (SNP).
                                  structure stored in the computer readable storage medium, the data structure including information resident in a database used by the application programme and including records, each record comprising information identifying a polymorphism shown in the above sequences. products and methods can be used for analysing polymorphic sites in individuals for testing for the presence of a disease phenotype or inforensics, paternity testing or genetic mapping of phenotypic traits. They can also be used for the production of polypeptides expressed by variant genes and for the production of transgenic animals. The nucleic segments can also be used in the manufacture of medicaments for the production of transgenic animals.
                                                                                                                                                                         Sequences AAX06101-X06558 represent human DNA fragments which contain biallelic polymorphic markers. The base occupying the polymorphic site indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in a method for determining polymorphic forms in an individual. The invention further provides computer-readable storage medium for storing data for access by an application programme being executed on a data processing system. Such a method comprises a data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                        Claim 1; Page 10;
                                                                                                                                                                                                                                                                                                                                New nucleic acid segments containing polymorphic sites - used for, e.g. detecting a disease phenotype, in forensics, paternity testing or genetic
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-080963/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phenotypic typing; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism; biallelic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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                                                                                                                                                                                                                                                                                                                   mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-1997;
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                            of diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forensic; genetic mapping;
ker; human; ss.
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RESULT 25
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Best Local
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                                                         05-OCT-1999;
                                                                                                25-AUG-2000;
                                                                                                                                          12-APR-2001
                                                                                                                                                                                                                                                             alternative
                                                                                                                                                                                                                                                                                  Human; RecQ5 alpha; RecQ5 beta;
                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                16-JUL-2001
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                    (AGEN-) AGENE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ31919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a PCR primer for DNA encoding the human he he invention, designated RecQ5. The helicase RecQ5 gene can be usenthod for the diagnosis of diseases caused by an abnormality case gene. The gene can be used in researching the relationship een the maintenance of human homeostasis and cell aging
                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                       RecQ5 alpha DNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding helicase, RecQ5 - onship to the maintenance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RecQ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                             splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                  2000WO-JP005757
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                                                           99JP-00284001
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                    INST CO LTD
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                     PCR primer 6F
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                                                                                                                                                                                                                                                                                RecQ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful in research for elucidating the of human homeostasis and cell aging.
                                                                                                                                                                                                                                                             instability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 U;
                                                                                                                                                                                                                                                             gamma; DNA helicase;
tability; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the human helicase
gene can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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RESULT 20
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, so matched the nucleic also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence of a method of analysis comprises of at least one target sequence.
                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a primer used to isolate a polynucleotide encoding a human RecQ5 type DNA helicase. The three RecQ5 type helicases alpha, beta and gamma are formed by alternative splicing. The invention discloses the RecQ5 type DNA helicases beta and gamma, and the genes encoding them. The RecQ5 beta DNA helicase has a novel characteristic of being localised in the nucleus. It is useful as a diagnostic marker or in
                                                                                                                                                                 New array of nucleic acid probes, useful for Southern, Northern or dot-blot hybridization sequence or specific mutations of any gene.
                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                       Mittmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST; ss; probe; ex
genetic variation;
                                                                                                                                                                                                                                                                                  (AFFY-)
                                                                                                                                                                                                                                                                                                           16-MAR-2001; 2001US-0276759P
                                                                                                                                                                                                                                                                                                                                      15-MAR-2002; 2002US-00098263
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                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cross-species comparison.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human microarray DNA oligonucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACI25999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACI25999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              being localised in the nucleus. It is useful as a diagnostic mark the treatment of diseases associated with chromosomal instability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding treatment of chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Furuichi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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15; Conserv
                                                                                                                                                                                                                                                                                 AFFYMETRIX INC
                                                                                                                                         SEQ ID NO 25990; 9pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTATGGAATGATACCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCATGGAATGATCCTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 5 A; 6 C; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; microarray,
n; biallelic marker; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
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l instability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.2; DB 4;
Pred. No. 5.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for diagnosis
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expression profile of a cancer cell, predicting the effect of a cytotoxic agent on a cancer cell obtained from a mammalian subject and identifying/characterizing an agent that modulates the expression or activity of one or more chemosensitivity genes. The array and methods are useful for identifying the chemosensitivity gene profile of a cancer cell or for determining the chemosensitivity of cells to cytotoxic agents. These may also be used for identifying and characterizing new agents that modulate the chemosensitivity of cancers. The present sequence is a control probe used in the microarray of the invention, an RGS (not

The invention relates to an array for determining the chemosensitivity of a cancer cell to a particular agent comprising a population of polynucleotide probes designed to be complementary to and hybridize under stringent conditions with a target region of at least one gene listed in the specification, where at least one of the polynucleotide probes is a control probe. Also included are detecting a chemosensitivity gene expression profile of a cancer cell, predicting the effect of a cytotoxic

Query Match Best Local (

Sequence

70 control.

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14 G;

20 T; 0 U; 0 Other;

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Mismatches

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Similarity

68.0%;

Score 13.6; Pred. No. 46

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RESULT 22
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microorganisms using at least one of 1138 oligonucleotide probes fully defined in the specification. The method is especially used to detect beverage-spoiling microorganisms in alcohol-free beverages, for example fruit-based drinks or water, but may also be extended to analysis of soil, plant parts, waste water, silage, clinical samples (feces, blood or tissues), foods, cosmetics and pharmaceuticals. The method provides rapid (1-2 days, compared to up to 10 days for classical culture methods) and specific detection of spoilage microorganisms. It combines the advantages of classical fluorescent in situ hybridization with those of culture
                                                                                                                                                                                           Detecting alcoholic,
                                                                                                                                                                                                                                                                                                                            23-SEP-2003; 2003DE-01044057
                                                                                                                                                                                                                                                                                                                                                         23-SEP-2004; 2004WO-EP010695
                                                                                                                                                                                                                                                                                                                                                                                                                   WO2005031004-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         food; microorganism detection; microorganism identification; water
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beverage-spoiling microorganism detection-related oligo probe SeqID270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADZ17963;
                                                                                                                                    This
                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                 Snaidr J,
                                                                                                                                                                                                                                                                                                                                                                                      07-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             waste-water;
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                                                                                                                                                                                                                                                                                                (VERM-) VERMICON
                                                                                                                                    invention
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                                                                                                                                                                SEQ ID NO 270;
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                                                                                                                                                                                          spoilage microorganisms in beverages, particularly non-
, by hybridization testing with specific oligonucleotides
                                                                                                                                                                                                                                                                   Beimfohr C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe; ss; DNA detection
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                                                                                                                                    relates to
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                                                                                                                                   a novel method for detecting
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RESULT 24 AAZ31919

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RESULT 23
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Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methods, can differentiate between closely related organisms, is suitable for screening large numbers of samples and allows simultaneous detection of several different microorganisms. The present sequence is that of an oligonuclectide probe which may be used for detecting beverage-spoiling microorganisms in the method of the invention.
                                                                                                                                                                                                The invention relates to a human gene RecQ4 encoding a protein having helicase activity. The gene has significant homology to the Escherichia coli helicase gene (RecQ). Host cells transformed with vectors comprising the RecQ4 gene are used for the recombinant expression of the protein.

The recombinant expression of the protein which recombinant expression of the protein in which we have a simple control of the study and diagnosis of disorders in which recombinant expression of the protein in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and diagnosis of disorders in which recombinate the study and disorders in which recombinate the study and disorders in which recombinate the study are study as the study and disorders in which recombinate the study are study as the study and disorders in which recombinate the study are study as the study as the study as the study are study as the study as the
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                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                            Disclosure; Page 55; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                    New human helicase gene RecQ4 helicase-implicated diseases s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimamoto A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-1999.
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                                                               Similarity
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                                                                                                                          24
                                                                                                                                                                                 may be used for the study and diagnosis of activity is involved, such as Werner's and
  TTATGGAATGATACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 2 A;
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                                            Conservative
                                                                                                                          BP; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitao S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                        A; 6 C; 6 G; 7 T; 0
                                                                                                                                                                the
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                                                           66.0%;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Werner's syndrome; Bloom's syndrome; human
                                                                                                                                                            helicase gene are implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CO LTD
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No. 5.6e+03;
                                                                                                                                                                                                                                                                                                                                                                       such
                                                                                  Score 13.2;
                                                                 Pred.
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                                                                 No.
                                                                                                                                                                                                                                                                                                                                                                    for investigation and Werner's syndrome.
                                                                                                                          U; 0 Other;
                                                                 5.7e+03
                                                                                    DB 2;
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                                                                                    Length 24;
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                                                                                                                                                                                                                                                                                                                                                                                              diagnosis
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Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukocyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
                      Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of the gene and placing other allele of the gene under conditional expression
                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2001; 2001WO-US049486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fungus; yeast; tetracyclin;
signal transduction; DNA rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides.
                                                                                                                                                                                                                                                                    22-AUG-2001;
                                                                                                                                                                                                                                                                                                                  29-DEC-2000;
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Claim 27; Fig 8; 136pp; English

to cytotoxic agents.

resistance

e f

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target

g

agent of a of a

WPI; 2004-043125/04

Identifying nucleic acid ligand of target molecule from mixture comprising single stranded nucleic acids having region of randomized sequence by contacting mixture with target molecule, amplifying affinity nucleic acids.

Electrophoresis-Systematic Evolution of This invention relates to a novel method

SEQ

ID NO 47; 90pp; English.

lectrophoresis-Systematic Evolution of Ligands by EXponential nrichment) of identifying nucleic acid ligands of a target molecule from candidate mixture comprised of single stranded nucleic acids each

(CE-SELEX,

Capillary

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RESULT 18
AAZ67315
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Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chemistry, useful in wide range of diagnostic assays and as direct benefits to many area of the research, including biomedical and health research improved apramers are useful in developing diagnostic assays, for example as diagnostic markers in medical analysis, in vivo imaging and biosensors. The aptamers are also useful in quantitating targets present in complex matrices. The aptamers are used to develop highsensitivity affinity probe capillary electrophoresis (APCE) assays, in BLISA type assays using enzyme-linked DNA aptamers. Thrombin aptamers me developed for using fibre-optic microarray biosensors. Aptamers against transformed endothelial cells may be selected for use as histological markers to identify tumour microvessels. Aptamers may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         having a region of randomised sequence by contacting the mixture with the target molecule, where nucleic acids having affinity to the target molecule are partitioned from the mixture by capillary electrophoresis, amplifying increased affinity nucleic acids to yield a ligand-enriched mixture of nucleic acids. The invention may be useful for the production of compounds with an antiasthmatic, cerebroprotective, anti-HIV or virucide activity. The method is useful for identifying nucleic acid ligands of a target molecule from a candidate mixture comprised of single stranded nucleic acids each having a region of randomised sequence. Aptamers identified by the method are useful as a tool in analytical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developed for use in other aptamer-based assays, such as assays for analytes ranging from anthrax spores to cocaine. Aptamers having improved quality, improved binding efficiency and selectrivity can be identified by the method of the invention. The present sequence is that of an aptamer DNA sequence which was identified using the method of the invention.
                                                                                                                                                                                                                                                          Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haplotyping; hybridisation; identification; characterisation; displaying; hybridisation; displaying; by high statements of the second seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ67315 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                       Human map-related biallelic marker SEQ ID NO:1662
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-2001
                                                                                       variation
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                    nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGAATGATACCGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATCGATACCGTCAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                            biallelic marker; high density disequilibrium map;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                     Location/Qualifiers replace(24,G)
/*tag= a
                            standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                       polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 24 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%;
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using the
                                                                                                                                                                                                                                             вр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                          diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                      Matches
                                                                                 Query Match
                                                                                                                                                                                             AAZ65654 to AAZ69578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AAZ69579 to AAZ77440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haplotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from
                                                                                                            Sequence
                                                                                                                                                    pharmaceutical agents acting on a disease as well as other treatment. N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 an 3367, are not actually given a sequence in the Sequence Listing from
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 585; 2745pp;
                                                                                                                                                                                                                                                                                                                                                                                                 map
                                                                                                                                                                                                                                                                                                                                                                                                                Novel biallelic markers
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1998;
23-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9954500-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cohen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST )
                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                  0f
                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-013267/01.
 27
                                                      16;
                          ш
                                                                     Similarity
                                                                                                                                           invention
                                                                                                               47
                            TTATGGAATGATACCGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blumenfeld
                                                      Conservative
                                                                                                               BP; 18 A; 4 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0082614P
98US-0109732P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-IB000822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ξ,
                                                                    68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chumakov
                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                        English.
                                                        0;
                                                                    Score 13.6; DB 3;
Pred. No. 3.8e+03;
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                                                                                                               <u>ი</u>
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                construct a high
                                                                                                               15 T; 0 U; 0 Other;
                                                                                 Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                 density
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 disequilibrium
                                                         0
                                                         Gaps
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RESULT 19
ABZ03677
TO PROCESS OF STREET
                                                                                                                      T7; leukocyte; gene expression profiling; allograft rejection; atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
         20-OCT-2000;
08-JUN-2001;
                                                                                                                                                             Human
                                                                                                                                                                               09-JAN-2003
                                                                                                                                                                                                  ABZ03677;
                                                                                                                                                                                                                    ABZ03677 standard; DNA;
                                                                          WO200257414-A2
                                                                                             Homo
                                    22-OCT-2001; 2001WO-US047856
                                                       25-JUL-2002
                                                                                                                                                             leukocyte
        2000US-0241994P.
2001US-0296764P.
                                                                                                                                                                               (first entry)
                                                                                                                                                            gene
                                                                                                                                                            expression
                                                                                                                                                                                                                      50
                                                                                                                                                                                                                      ВP
                                                                                                                                                             profiling
                                                                                                                                                              probe
                                                                                                                                                              SEQ
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RESULT 16
AAD39720/c
ID AAD397
XX AAD397
XX Synthe
AC Synthe
XX Synthe
XX Membra
KW Hydrog
KW biotec
KW biotec
KW biosep
XX Uniden
XX Uniden
XX UNIGEN
XX UNIGEN
XX UNIGEN
XX UNIGEN
XX UNII
XX UNII
XX UNII
XX WPI; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a membrane scaffold protein (MSP), that self CC assembles in the absence of phospholipid, with a phospholipid or a CC mixture of phospholipids, into a nanoscale particle of 5-500 nm in CC diameter, in an aqueous environment, where the membrane scaffold protein CC comprising MSP is useful for identifying a competitor of binding of a CC ligand to a receptor protein which is incorporated within the nanoscale particle compound, and measuring detectable ligand released from the particle. CC bound detectable ligand, contacting the bound ligand with a test CC compound, and measuring detectable ligand released from the particle, CC such that a competitor of ligand binding is identified when contacting the bound ligand with a test CC compound; are sults in release of the detectable ligand. The CC invention is useful for the incorporation of additional hydrophobic or partially hydrophobic protein molecules. The nanoscale particle can form CC tags for purification and physical manipulation of disks such as in CC particle and MSP are useful in biotechnology, pharmaceutical industries for rapid and reproducible assay and crystallisation. The nanoscale cand in research areas. The nanoscale particle is useful for structure/ CC discovery. The present sequence is a synthetic oligonucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 15
   New membrane scaffold protein
                                                                  Sligar
                                                                                                                                                                        20-NOV-2001; 2001WO-US043451
                                                                                                                                                                                                           23-MAY-2002
                                                                                                                                                                                                                                             WO200240501-A2
                                                                                                                                                                                                                                                                                                                                                                                               Synthetic oligo taps3b used to construct synthetic MSP gene.
                                                                                                                                     20-NOV-2000; 2000US-0252233P
                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                              bioseparation;
                                                                                                                                                                                                                                                                                                                                biotechno.
                                                                                                                                                                                                                                                                                                                                              hydrogel;
                                                                                                                                                                                                                                                                                                                                                                 Membrane scaffold protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD39720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New membrane scaffold protein for forming nanoscale particles, useful in biological research, self assembles with(out) phospholipids into a nanoscale particle in an aqueous environment.
                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD39720 standard; DNA; 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example
                                    2002-500201/53
                                                                      SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                       VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Page 40; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGAATTATATCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGAATGATACCGTCA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                ; 7601
                                                                                                                                                                                                                                                                                                                                              gold biosensor surface;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetic MSP gene
                                                                      Bayburt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                       ILLINOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                            pharmaceutical industry; structure drug discovery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Þ
                                                                      보
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 C;
                                                                                                                                                                                                                                                                                                                                                                 MSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   股
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.8; DB 6; Pred. No. 3.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>ი</u>
 for forming nanoscale particles, useful
                                                                                                                                                                                                                                                                                                                                          phospholipid; nanoscale particle;
e; reproducible assay; crystallisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1e+03;
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ATGGAATGATACCGTCA

19

Matches Query Match

Local

l Similarity

Conservative

0;

Mismatches

0

Gaps

0

69.0%; 88.2%;

Score 13.8; Pred. No. 3

.2e+03;

Length Indels

Sequence

80 BP; 13

A; 23 C;

19

G.

25 T; 0

u; 멂

0 Other; 6,

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cc is amphipathic and forms at least one alpha helix. The nanoscale particle comprising MSP is useful for identifying a competitor of binding of a cc ligand to a receptor protein which is incorporated within the nanoscale particle together with MSP, by contacting nanoscale particle and a creeptor protein with a detectable ligand to produce nanoscale particle and creeptor protein with a detectable ligand to produce nanoscale particle. Cc compound, and measuring detectable ligand released from the particle, cs with that a competitor of ligand binding is identified when contacting cthe bound ligand results in release of the detectable ligand. The creeptor particle is useful for the incorporation of additional hydrophobic or partially hydrophobic protein molecules. The nanoscale particle can form cc tags for purification and physical manipulation of disks such as in the particle and MSP are useful in biotechnology, pharmaceutical industries can discovery. The present sequence is a synthetic oligonucleotide used to constation and drug constation and drug the present sequence is a synthetic oligonucleotide used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a membrane scaffold protein (MSP), that self assembles in the absence of phospholipid, with a phospholipid or a mixture of phospholipids, into a nanoscale particle of 5-500 nm in diameter, in an aqueous environment, where the membrane scaffold protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biological research, self assembles with(out) phospholipids into nanoscale particle in an aqueous environment.
                                               construct synthetic MSP
                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
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RESULT 17
ADM79905/c
ID ADM79
XX ADM79
XX ADM79
XX DNA J
YX CB-SI
KW CB-SI
KW antit
KW antit
KW antit
KW antid
KW antid
XX Unid
XX Unid
OS Syntl
XX Unid
OS Syntl
XX Unid
Syntl
XX HUMON
XX UNID
XX UN
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                                               Bowser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CE-SELEX; capillary electrophoresis; ligand-enriched mixture; antiasthmatic; cerebroprotective; anti-HIV; virucide; analytical chemistry; in vivo imaging; biosensor; complex matrix; affinity probe capillary electrophoresis; APCE; ELISA; fibre-optic microarray biosensor; histological marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004
                                                                                                                                                                                                            31-MAY-2002;
15-MAY-2003;
                                                                                                                                                                                                                                                                                                                                         29-MAY-2003; 2003WO-US016796
                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003102212-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                             (MINU ) UNIV MINNESOTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA ligand identification-related aptamer DNA sequence SeqID47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                               Ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microvessel;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGAATTATATCGTCA
                                               Mendonsa SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                2002US-0384709P
2003US-0470750P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anthrax spore;
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Claim 15; SEQ ID NO 7536; bronchodilating agent

763pp; English.

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CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a composition of useful for preventing or cc treating a respiratory, lung or malignant disease. The administered cc composition comprises oligo and is administered to reduce the production cc availability, or to increase the degradation of the target mRNA or to creduce the amount of target polypeptide present in the lungs. The cpulmonary obstruction, and/or bronchoconstriction and/or lung cc inflammation, allergies and/or surfactant hypoproduction are associated confinemation, allergies, asthma, impeded respiration, respiratory cc inflammation, allergies, asthma, impeded respiration, respiratory cc inflammation, allergies, asthma, impeded respiration, respiratory cc hypothesison, emphysema, chronic obstructive pulmonary disease, pulmonary ctransplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to cthymidines present in the target RNA serves to prevent the breakdown of cc the oligonucleotides into products that free adenosine into the system ce.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to corresponding to the anti-sense oligos or breakdown of constant of the anti-sense oligos corresponding to the oligonucleotides into products that free adenosine into the system cc.g. rung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallargic, antiinflammatory, antiasthmatic.
                                                                                                                                                                                                                                                                                                   ss; primer; antibacterial; antiinflammatory;
gene therapy; diagnosis; sexually transmitted
respiratory disease; pneumonia; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae gene reverse PCR primer #79
                                                                                                                                                                                                                                                                                                                                                                                                                                     18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR99683 standard; DNA; 30
                                                                                  24-FEB-2003; 2003US-0448879P
                                                                                                                                                                                                                 WO2004074318-A2
                                                                                                                                                                                                                                                          Chlamydophila pneumoniae
                                                                                                                             24-FEB-2004; 2004WO-IB000902
                  (INSP ) INST PASTEUR.
(CNRS ) CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       μ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                            diagnosis; sexually transmitted disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 A; 4 C; 3 G; 5 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%;
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Pred. No. 2
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1.7e+03;
                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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artivity, is a
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WPI; 2002-500201/53

20-NOV-2000; 2000US-0252233P 20-NOV-2001; 2001WO-US043451

(UNII ) UNIV ILLINOIS FOUND

Bayburt

WO200240501-A2 Unidentified.

23-MAY-2002

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RESULT 15
AAD39714
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The invention relates to a purified secreted Chlamydia polypeptide or its cragment. The Chlamydia polypeptide is homologous to one or more chlamydia pneumoniae proteins selected from CPn0104, CPn0210, CPn0399, CPn0405, CPn0443, CPn0480, CPn0489, CPn0490, CPn0497, CPn0522, CPn0399, CPn0582, CPn0588, CPn05895, CPn0671, CPn0673, CPn0681, CPn0712, CPn0720, CPn0725, CPn0729, CPn0729, CPn0729, CPn0729, CPn0729, CPn0746, CPn0770, CPn0714, CPn0779, CPn0879, CPn0879, CPn0879, CPn0939, CPn1002, CPn1005, CPn1007, CPn10019, CPn1002, CPn1002 and CPn1068. Alternatively, CPn1005, CPn1007, CPn1019, CPn1002, CPn1003 and CPn1068. Alternatively, CPn1004, CPn1070, CPn1005, CPn1007, CPn1019, CPn1002, CPn1032 and CPn1068. Alternatively, CPn1005, CPn1007, CPn1019, CPn1003, CPn1032 and CPn1068. Alternatively, CPn1005, CPn1007, CPn1019, CPn1032 and CPn1068. Alternatively, CPn1005, CPn1007, CPn1019, CPn1003, CPn1003, CPn1003, CPn1003, CPn1002, CPn1003, CPn1003
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                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane scaffold protein; MSP; phospholipid; nanoscale particle; hydrogel; gold biosensor surface; reproducible assay; crystallisation; biotechnology; pharmaceutical industry; structure determination; bioseparation; drug discovery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic oligo taps3a used to construct synthetic MSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD39714 standard; DNA; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing and treating Chlamydia infections, such as sexually transmitted diseases, respiratory diseases (e.g. pneumonia or bronchitis) or atherosclerosis. The may also be used in drug screening purposes. This sequence corresponds to a PCR primer to amplify one of the Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 111; SEQ ID NO 328; 210pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 BP; 9 A; 6 C; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGCAATGATATCGTCA 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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RESULT 1:
ABZ92294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a bacterial strain, particularly an Escherichia CC coli strain for the secretion of soluble, biologically active recombinant heterologous proteins into the periplasm or culture medium. The bacterial strain expresses a fusion protein comprising a signal peptide, a mature heterologous protein, and a bacterial surface protein subunit simultaneously with a periplasmic chaperone and an outer membrane protein cusher/secretin protein, both of which are specific for the surface protein subunit component of the fusion protein. In particular, the signal peptide and surface protein subunit are from the Yersinia pestis CC signal peptide and surface protein subunit are from the Yersinia pestis CC signal peptide and surface protein subunit are from the Yersinia pestis CC signal peptide and surface protein subunit are from the Yersinia pestis CC strain of the invention is useful for producing heterologous recombinant protein such as granulocyte macrophage-colony stimulating factor (GM-CSF), interleukin-1-beta (IL-1-beta), and IL-1 receptor antagonist (IL-CC lra). The present sequence represents a Yersinia pestis CafIM PCR primer county and in an exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                            Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
             corresponding ubiquinone.
                         Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                  24-APR-2001; 2001US-0286137P
                                                                                                                                                                                                                                                  23-APR-2002; 2002WO-US013135.
                                                                                                                                                                                                                                                                                   31-OCT-2002
                                                                                                                                                                                                                                                                                                                  WO200285308-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human oligonucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial strain simultaneously expressing a fusion protein, signal peptide-heterologous protein-subunit of bacterial surface structure, and periplasmic chaperone specific for recombinant heterologous protein.
                                                                                                                                                                                                                                                                                                                                                   Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ92294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ92294 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                 EPIGENESIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Page 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACGGAATGGTACCGACA 3
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                                                                                                                               Li Y,
Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTATGGAATGATACCGTCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                               Sandrasagra A,
L, Shahabuddin
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                                                                                                                                                                                                                                                                                                                                                                                respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.0%;
84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                  disease; ds
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                                                                                                                                              'n
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                                                                                                                                                Pabalan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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xx_0
                                                                      Contribution codon, coding region, 5' or 3' end genomic flanking regions, cc 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of cc junctions of genes encoding a polypeptide associated with lung and/or cc nasal airway dysfunction and a second active agent comprising an cc antiinflammatory steroid and ubiquinone. A composition of the invention cc antiinflammatory, antiallergic, antiasthmatic, hypotensive, c immunosuppressive, and cytostatic activity. The composition may have a cc use in antisense gene therapy. The composition is useful for treating or cc preventing a respiratory, lung or malignant disease or condition, also cc for enhancing the prophylactic or therapeutic respiratory effect of an cc antiinflammatory steroid in a subject, for reducing levels of adenosine cc for reducing sensitivity to adenosine, reducing levels of adenosine cc lung surfactant in a subject's tissue, or treating bronchoconstriction, cc lung surfactant in a subject's tissue, or treating bronchoconstriction, cc sinflammation, lung allergies, or a respiratory disease or condition. Cc Specification, but was obtained in electronic format directly from WIPO or treating treating bronchoconstriction, in the composition of the printed specification, but was obtained in electronic format directly from WIPO or treating the prophylactic or the sequence data for this patent is not represented in the printed or the composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   first active agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7536; 872pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vel pharmaceutical composition, an oligonucleotide antisense to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which
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Query Match
Best Local S
Matches 15
               w
                               l Similarity
               ATGGAATGATACCGTCAT
ATGGAATTAAACCGNCAT
                               Conservative
                                     69.0%;
18
               20
                              0;
                                      Score 13.8;
Pred. No. 2
                               Mismatches
                                       2.7e+03
                                             DB 10;
                                             Length
                              Indels
                                              20;
                              0
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0

뭐 S

Sequence

20 вÞ;

7 A; 4 C; 3

G; 5 T;

0 U; 1 Other;

RESULT 13
ABD28524
ID ABD28 R14663-derived oligonucleotide ABD28524 29-JUL-2004 standard; (first entry) DNA; 20 SEQ ID 7536.

respiratory distress syndrome; allergic rhinitis; emphysema; chronic obstructive pulmonary disease; pulmonary transplantation rejection; ss; primer. beta-adrenergic agonist; respiratory disease; pulr respiratory distress syndrome; allergic rhinitis; Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; pulmonary vasoconstriction; tis; pulmonary hypertension; ase; cancer; bronchitis;

WO200285309-A2

31-OCT-2002

23-APR-2002; 2002WO-US013143

24-APR-2001; 2001US-0286036P

(EPIG-) EPIGENESIS PHARM INC

တ Li 1. Tang ) ŗ Sandrasagra A, Shahabuddin ŝ Katz [H Pabalan ŗ Ü

Pharmaceutical composition for oligonucleotide containing les for treating asthma, has antisense less percentage of adenosine, targe ith lung airway or lung dysfunction. 6

· Service Statement

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RESULT 10
AAT86857/c
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                  PCR primers DruGen5' (AAT86744) and DruGen3' (AAT86745) are based on a raspberry drul cDNA sequence (see AAT86743). They were used in the PCR amplification of raspberry leaf genomic DNA. A drul genomic clone (see AAT86746) was obtained. Inverse PCR (see (AAT86747-48) was then used to isolate a genomic clone (see AAT86749) that included the drul 5' flanking region. The drul promoter (see AAT86739) is used in claimed chimeric genes for the high-level, tissue-specific expression of heterologous sequences in transgenic plants, especially to modify ethylene productions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  co-suppression; thaumatin; sweetener; sucrose phosphate synthase; lycopene cyclase; polygalacturonase inhibiting protein; glucanase; chitinase; PCR; primer; ss.
                                                                                                                     Promoter; drul; drul10; dru259; drupel; raspberry; transgenic plant; tissue-specific gene expression; neomycin phosphotransferase; hygromycin phosphotransferase; bromoxynil-specific nitrilase; selectable marker; herbicide resistance; fruit; primer; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant fruit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9727308-A1
                                                                                                                                                                                                                                 AAT86857
                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 7 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 33; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-393694/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubus idaeus
29-JAN-1996;
24-JAN-1997;
                                                  31-JUL-1997
                                                                                                   Synthetic
                                                                                                                                                                      Raspberry
                                                                                                                                                                                          09-FEB-1998
                                                                                                                                                                                                              AAT86857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AGRI-) AGRITOPE INC.
                                                                    WO9727307-A1
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                         idaeus.
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                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ethylene production.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JA,
                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                   TTATGCACTAATACCGTCA
                                                                                                                                                                                                                                                                                                       TTATGGAATGATACCGTCA 19
                                                                                                                                                                     drul gene PCR
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            especially raspberry, drul promoter - useful for high level, fic expression of heterologous sequences, especially to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bestwick
                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00592936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US001443.
96US-00592936
97US-00788928
                              97WO-US001275
                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                   71.0%;
84.2%;
                                                                                                                                                                      primer DruGen3'
                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                      Score 14.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                       1.7e+03
                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                    5' flanking
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RESULT 11
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial expression system, periplasmic secretion; Escherichia coli Yersinia pestis Cafi, periplasmic chaperone CafiM; Yersinia pestis Cafi, periplasmic chaperone CafiM; usher/secretin protein CafiA; IL-1-beta; interleukin-1-beta; GM-CSF; granulocyte macrophage-colony stimulating factor; IL-1ra;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yersinia pestis CaflM periplasmic chaperone PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC87300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC87300 standard; DNA; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raspberry promoters drul, drull0 and dru259 - used for genetic engineering of plants, e.g. to provide moderate expression of marker allowing growth in presence of selective agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kellogg
WPI; 2001-007229/01
                                                                                                                                                                                                                                          03-MAY-2000; 2000WO-FI000387.
                                                                                                                                                                                                                                                                          09-NOV-2000
                                                                                                                                                                                                                                                                                                          WO200066756-A1
                                                                                                                                                                                                                                                                                                                                        Yersinia pestis.
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                                                                                                                                                                                                           04-MAY-1999;
                                Korpela T,
Petrovskaya
                                                                                                                            (MACI/)
(ZAVI/)
(BATT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  госат
                                                                                                                                                                                                                                                                                                                                                                        primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                  receptor antagonist; fusion gene; fusion protein; junction region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                            MACINTYRE-AYANE S
ZAVIALOV A V.
BATTCHIKOVA N V.
PETROVSKAYA L E.
KOROBKO V G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Page 56; 84pp; English.
                                                                                KOROBKO V G.
ZAV'YALOV V P.
                                                                                                                                                                             KORPELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATGCACTAATACCGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTATGGAATGATACCGTCA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 7 A; 4 C;
                                Macintyre-Ayane
LE, Korobko VG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bestwick
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84.2%;
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Pred. No. 1.7e+03;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 T;
                                 Zav' yalov
                                   Zavialov AV,
av'yalov VP;
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••
                                                  Battchikova
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RESULT 8
ADT55403/c
ID ADT554
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                                                                                                                                                                                                                                                           CC sequence encoding the catalytic or substrate-binding domain of a comprising the activity of the polypeptide of SEQ ID NOS: 261-497, where the polypucleotide encodes a polypeptide having the activity of the polypucleotide of SEQ ID NOS: 261-497 (c) or (1ii) a nucleic acid sequence of SEQ ID NOS: 471-697. Also described are: (1) a DNA construct comprising at least one polynucleotide having the sequence of SEQ ID NOS: 1-237 or their conservative variants; (2) a cplant cell transformed with the DNA construct of (1); (3) a transgenic plant cell transformed with the DNA construct of (1); (3) a transgenic tree which has been transformed with the DNA construct of (1); (6) a comprising an amino acid sequence encoded by the new isolated polypucleotide or comprising any of the amino acid sequences of SEQ ID NOS: 261-497; (8) a method of altering a plant phenotype of a plant; (9) a method of correlating gene expression in two different samples; (10) a method of correlating the possession in two different samples; (10) a combination, for detecting expression of a plant phenotype to the level of combination, for detecting expression of one or more genes; (11) a method of correlating to a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene expression in the plant of one or more genes, comprising the product encoded by a nucleic acid sequence of SEQ ID NOS: 1-237 or to gene product encoded by a nucleic acid sequence of SEQ ID NOS: 1-237, (13) a composition on the solid support, (14) a method for detecting one or more genes a unique composition on the solid support, (14) a method for detecting one or more coled not one or more coled by the formences encoded by one or more genes in a sample; (15) a method of corrected by one or more of combination of (12) provided on a solid constraint of the two or more of combination of the coled action on the solid support; (14) a method for detecting one or more mucleic acid coled sequence of sequence of sequence more mucleic acid coled sequence of sequence of sequence of sequence of se
                                                                                                                                                                           Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                 genes in a sample; (15) a method for detecting one or more nucleic aci sequences encoded by one or more genes in a sample; and (16) a kit, for detecting gene expression, comprising the microarray of (13) together with one or more buffers or respents for a nucleit of hybridization
  ADT55403 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forster I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005065339-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pinus radiata
                                                                                                                                                                                                                                                                                          ction. The polynucleotides, polypeptides, DNA construct, composition, methods are useful for modifying plant development and altering plant notype. This sequence represents an oligonucleotide used in the ation of a microarray for detection of cell cycle genes.
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                                                                                                                                                                             18;
                                                                                                                                                                                              Similarity
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GENESIS RES
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                                                                                                TTATGGAAAGATACGGTCAT 25
                                                                                                                                    TTATGGAATGATACCGTCAT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of SEQ
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                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   describes an isolated polynucleotide comprising: (i) a EQ ID NOS: 1-237 or their conservative variants; (ii) a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556; 499pp; English.
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                                                                                                                                                                                            84.0%;
90.0%;
                                                                                                                                                                                                                                                           12 C;
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czycki RJ;
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and altering
                                                                                                                                                                           Pred. No. 80;
0; Mismatches
                                                                                                                                                                                                                  Score 16.8;
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                                                                                                                                                                                                                                                       21 T; 0
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plant
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                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                         0 Other;
                                                                                                                                                                         <u>ب</u>
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                                                                                                                                                                                                                Length
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RESULT 9
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EVALUATION OF TEB
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Promoter; drul; raspberry; transgenic plant; fr
tissue-specific gene expression; ethylene;
S-adenosylmethionine hydrolase;
aminocyclopropane-1-carboxylic acid deaminase;
aminocyclopropane-1-carboxylic acid oxidase; AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a nucleic acids and polypeptides encoding four novel splice variant isoforms of human histone deacetylase (HDAC3). The human HDAC3 nucleic acid is useful as hybridisation probes or PCR primer for identifying nucleic acids encoding for proteins related to histone deacetylase, or for the recombinant expression of histone deacetylase. The HDAC3 polypeptides are useful for enhancing an immune response and modulating transcription activity or levels of histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human histone deacetylase 3 nucleic acid, useful as hybridization probes or PCR primer for identifying nucleic acids encoding for proteins related to histone deacetylase, or for the recombinant expression of
                                                                                                                                              PCR primer DruGen3' used for drul genomic DNA amplification.
                                                                                                                                                                                                  05-FEB-1998
                                                                                                                                                                                                                                                  AAT86745
                                                                                                                                                                                                                                                                                                 AAT86745 standard;
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HDAC3sv1.2 spe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conserv
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LOERCH P M.
CASTLE J C.
JOHNSON J M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                       TTGTGGAAGGACACCGTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 31;
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2003US-0478233P
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                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                entry)
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85.0%;
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3;
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  e; ACC deaminase;
ACC oxidano
    oxidase; antisense;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                         methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic disorder. The invention is also useful in antisense-therapy. The present sequence is human histone deacetylase 2 DNA antisense oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense oligonucleotide compound, useful for diagnosing, preve and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-2002; 2002US-00173192
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                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example
              Histone deacetylase 2; HDAC2; HDAC-2; hdac2; RPD3; hRPD3; hyperproliferative disorder; cancer; antisense gene thera antisense; phosphorothioate backbone; ss.
                                                                                        15-JUL-2004
                                                                                                                                         ADN49063 standard;
                                                                                                                                                                                                                                                                                                                                 exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC
             hyperproliferative disorder; antisense; phosphorothioate
                                                               Human HDAC2 specific antisense oligo,
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                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                      20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                      95.0%;
llarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                 of the invention.
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5-methyl cytidines"
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== "2'-methoxyethyl
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                                                                 ISIS 157265.
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antisense compounds, compositions and methods for modulating the expression of histone deacetylase 2 (HDAC2). HDAC2 also known as HDAC-2, hdac2, human RPD3 and hRPD3. The composition comprises antisense compounds that can be targeted towards HDAC2. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New compound, having a sequence targeted to a coding region of a nucleic acid encoding human histone deacetylase 2, useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer.
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                                                                         plant protectant; fungicide; plant growth regulant; gene therapy;
cell cycle; gene expression; plant; transgenic plant; microarray; wood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; SEQ ID NO 34; 47pp; English.
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/note= "Phosphorothioate backbone in which all cytidines
are 5-methylcytidines"
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/note= "2'-methoxyethyl bases"
16. .20
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                                                                                                                                                                                 Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound, having a sequence targeted to a coding region of a nucleic acid encoding human histone deacetylase 2, useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN49062 standard;
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DOBIE K W.
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                15; SEQ ID NO 33; 47pp; English
                                   TTATGGAATGATACCGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dobie KW;
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                                                                                                                                                                                 B₽;
                                                                                       Conservative
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/note= "Phosphorothioate backbone in which all
are 5-methylcytidines"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New compound, having a sequence targeted to a coding region of a nuc acid encoding human histone deacetylase 2, useful for preparing a composition for treating hyperproliferative disorders, e.g., cancer.
   Homo sapiens
                                                                      phosphorothioate
                                                                                                                                                                                                                                                          Human histone
                                                                                                                                                                                                                                                                                                                                 20-MAY-2004
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                                                                                                        hyperproliferative disorder; antisense-therapy; cytostation
                                                                                                                                                                                   Histone deacetylase 2; HDAC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 15; SEQ ID NO 61; 47pp;
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                                                                                                                                                                                                                                                  deacetylase 2 DNA antisense oligo,
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                                                                          backbone; antisense; ss.
                                                                                                            cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorder;
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                                                                                                                                          cancer;
                                                                                                 diagnosis; prevention;
cancer; apoptosis; metabol
; antiinflammatory; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB
Pred. No. 1.4;
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                                                                                                                                             disorder;
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                                                                                                                                                                                                                                                                                                                                                                                   Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperproliferative disorder; cancer; apoptosis; meta
                                                                                                                                                                                                                                                                                                                                      modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ27016 standard;
                           The present invention relates to antisense compounds, compositions and methods used for modulating histone deacetylase 2 (HDAC2). The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with
                                                                                          New antisense oligonucleotide compound, useful for diagnosing, and/or treating conditions with aberrant activity of the histor deacetylase 2, such as cancer, inflammation and metabolic disorder.
                                                                                                                                                                                           14-JUN-2002; 2002US-00173192.
                                                                                                                                                                                                              14-JUN-2002; 2002US-00173192
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aberrant expression or activity of histone deacetylase 2, such as hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic di
                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens
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                                                                           SEQ ID NO 33;
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/mod_ba
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/note= "Phosphorothioate
5-methyl cytidines"
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                                                                                                                                                         and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of histone deacetylase 2, such as a hyperprobliferative disorder (cancer)
                                                                                                                                                                                                                                                                        New antisense oligonucleotide compound, useful for diagnosing, p and/or treating conditions with aberrant activity of the histone deacetylase 2, such as cancer, inflammation and metabolic disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Histone deacetylase 2; HDAC2; diagnosis; prevention; hyperproliferative disorder; cancer; apoptosis; meta antisense-therapy; cytostatic; antiinflammatory; hum
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                                                                                                      The invention is also useful in a is human histone deacetylase 2 ta exemplification of the invention.
                                                                                                                     aberrant expression or accept, a condition involving an hyperproliferative disorder (cancer), a condition involving an inflammatory response or an aberrant apoptosis and a metabolic The invention is also useful in antisense-therapy. The present the invention is also useful in antisense-therapy are present the invention is also useful in antisense-therapy.
                                                                                                                                                                                                        The present invention relates to antisense compounds, methods used for modulating histone deacetylase 2 (HD
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Adn49090 Human his
Adn49093 Human his
Adn49093 Human HDA
Adb27395 P. radiat
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Aat 86747 PCR prime
Aat 8687 Raspberry
Aac87300 Yersinia
Abc22294 Human oli
Abd29524 R14663 de
Add29683 Chlamydia
Aad3970 Synthetic
Aad39705 DNA ligan
Aaz67315 Human
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ABV7586320
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ABT12857

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Adc742546 Common pr
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Ade40076 5' TET an
Aax59666 Phytase-1
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Adc400745 Site dire
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Aci53879 Human mic
Aaq85376 TRH recep
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TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome patent: US 6537751-A 1307 25-MAR-2003;

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AUTHORS
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                                synthetic construct
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other sequences, artificial sequences.
1 (bases 1 to 31)
Bachtoc, A., Mew, T. and Luckel, M.
Continuous fermentation step
Patent: JP 2001149480-A 29 29-MAY-2001;
F HOFFMANN LA ROCHE AG
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PN JP 2001145480-A/28
PD 29-MAY-2001
PF 11-OCT-2000 JP 2000311300
PF 11-OCT-1999 EP 99120289.6,08-SEP-2000 EP 00119676.5 P
ATYLA BACHTOC, TORSTEN MEW, MARCAS LUCKEL
PC C12N1/00,C12M1/36,C12N1/00//C12N9/16,C12N15/09,C12N15/00
Primer
PH Key Location/Qualifiers
FH Key 1..31
FT SOURCE /organism='Artificial Sequence'.
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Bachtoc, A., Mew, T. and Luckel, M.
Continuous fermentation step
Patent: JP 2001145480-A 28 29-MAY-2001;
F HOFFMANN LA ROCHE AG
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/db_xref="taxon:32630"
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PR 11-OCT-1999 EP 99120289.6,08-SEP-2000 EP 00119676.5 PI
ATYLA BACHTOC,TORSTEN MEW,MARCAS LUCKEL
PC C12M1/00,C12M1/36,C12N1/00//C12N9/16,C12N15/09,C12N15/00 CC
Primer
PH Key Location/Qualifiers
FT source 1. 31
FT source /organism='Artificial Securete'
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Sequence 33 from Patent
CQ816210
CQ816210.1 GI:48144567
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                                                                                    AR289572
Sequence 1307 from patent
AR289572
AR289572.1 GI:31676856
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Mammalia; Eutheria;
Unclassified.
1 (bases 1 to 47)
Cohen, D., Chumakov, I.
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                                             Unknown.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                 /note="Gal-NAc-T1 lectin domain forward primer"
                                                                                                                                                                                                                                                                                                                                                      /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
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Pred. No. 3.7e+05;
0; Mismatches 4
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Pred. No. 3.6e+05;
0; Mismatches 4;
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AUTHORS

and Blumenfeld, M.

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Unknown
                                      Sequence 52
AR494427
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Bartok, A., Mueh, T. and Rueckel, M.
Bartok, A., mueh, T. and Rueckel, M.
Continuous fermentation system
Patent: US 6599735-A 29 29-JUL-2003;
Roche Vitamins Inc.; Parsippany, NJ;
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AR361596
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Bartok, A., Mueh, T. and Rueckel, M.
Continuous fermentation system
Patent: US 6599735-A 28 29-UUL-2003;
Roche Vitamins Inc.; Parsippany, NJ;
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AR361595
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        Unknown.
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/mol_type="genomic
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/mol_type="genomic DNA"
                             GI:47268592
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from patent US 6599735.
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Pred. No. 3.7e+05;
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Best Local Similarity
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Sequence 29:
AX137178
                                                              Continuous fermentation process
Patent: EP 1092764-A 29 18-APR-2001;
F. HOPFMANN-LA ROCHE AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bartok, A., Mueh, T. and Rueckel, M. Continuous fermentation process Patent: EP 1092764-A 28 18-APR-2001; F. HOFFMANN-LA ROCHE AG (CH)

Location/Qualifiers
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Sequence 28 from Patent EP1092764.
AX137177
AX137177.1 GI:14273503
                                                                                                               Bartok, A., Mueh, T. and Rueckel, M.
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                                                                                                                                               other sequences; artificial sequences.
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1 (bases 1 to 31)
Lehmann, M.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
                                                   Location/Qualifiers
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/db_xref="taxon:32630"
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Pred. No. 3.7e+05;
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Pred. No. 3.7e+05;
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CS075741
Sequence 158
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Patent: WO 0145493-A 56 28-JUN-2001;
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Dorreich,K., Christensen,F.M., Schnell,Y., Mischler,M., Dalb.
Blashed,ge,H. and Heldt-Hansen,H.P.
Aspergillus aculeatus rhamnogalacturon acetyl esterases, DNA
sequences encoding the enzymes and methods of use thereof
sequences encoding the enzymes;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Sequence 5 from patent US
132151
132151.1 GI:1822942
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                                                                                                                                                                                        /mol_type="unassigned DNA"
                                                                                                                                                                                                     /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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             21 bp RNA
Patent WO2005036176.
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Pred. No. 2.6e+05;
0; Mismatches 2;
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Pred. No. 3e+05;
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PR 22-JAN-1999 DK PA 199900092,21-SEP-1999 DK PA 199901340 PI MARTIN LEMANN, SOANE FLENSTED LASSEN

PC C12N15/09,A23K1/165,A23L1/30,A61K38/46 ACCTORN 1/19,

C12N1/19,

PC C12N1/21 CTANAME PROPERTY OF ACCTORN 1/19,
29
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                      SURFE
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Lemann, M. and Lassen, S.F.
Improved phytases
Patent: JP 2002534976-A 22
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synthetic construct
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Patent: WO 2005036176-A 158 21-APR-2005;
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TTCTGGAATGATCACGTTA 11
                         TTATGGAATGATACCGTCA 19
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Description of Artificial Sequence:
Key Location/Qualifiers
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                                                                                                                                                                  /organism='Artificial
Location/Qualifiers
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/mol_type="unassigned RNJ
/db_xref="taxon:9606"
                                                                                                                  /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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78.9%;
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Pred. No. 3.7e+05;
0; Mismatches 4;
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Pred. No. 3.9e+05;
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                                                                     Oligonucleotide library for detecting rna variants that populate a transcriptome Patent: WO 0210449-A 17126 07-PEB-2002;
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Sequence 17126 from Patent CQ547491 CI:41513755
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Oligonucleotide library for detecting variants that populate a transcriptome Patent: WO 0210449-A 8391 07-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ538756
Sequence 8391 from Patent
CQ538756
CQ538756.1 GI:41505020
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
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                                                Location/Qualifiers
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 1.6e+05;
0; Mismatches 3
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Pred. No. 1.7e+05;
1; Mismatches 4
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Sequence 39
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AX054735.1
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Tumor-associated antigen (c42)
Patent: WO 0073438-A 39 07-DEC-2000;
BOEHRINGER INGELHEIM VETWEDICA GMBH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                      synthetic construct
synthetic construct
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TATGGAATGATACCGTCA 19
                                                                                                                                                                                                                                          other sequences; artificial sequences.
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Mammalia; Eutheria;
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                                                                                           /mol_type="unassigned
/db_xref="taxon:32630"
/note="Primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="unassigned DNI
/db_xref="taxon:9606"
                                                                                                                                  organism="synthetic construct"
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Pred. No. 1.6e+05;
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OS Artificial Sequence
PN WO 0125425-A/12
PD 12-APR-2001
PF 25-AUG-2000 WO 2000JP005757
PR 05-OCT-1999 JP 99P 284901
PI YASUHIRO FURUICHI, AKIRA SHIMAMOTO, SAORI KITAO, KAORI NISHKAWA
PC C12N15/12, C12N9/14, C12Q1/68, C07K16/18, G01N33/53, A01K67/00 CC
Description of Artificial Sequence: Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers.
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Sequence 738 from Patent
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BD012839.1 GI:22093028
WO 0125425-A/12.
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24 bp DNA
Nucleus localizing RecQ5-type DNA helicase.
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Brower, A.,
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nilarity 83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
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  Brow, M.A., Cracauer, R.F., Fors, L.,
                                                                                                                                                                  GI:28398640
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Systems and method for detection assay production and sale Patent: WO 0244994-A 766 06-JUN-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)

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Mammalia; Eutheria;
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          Nakamura, Y., Sekine, A., Iida, A. and Saito, S. Detection of genetic polymorphisms Patent: WO 02052044-A 4375 04-JUL-2002;
                                                                                                                                                                     Sequence 4375 from Patent AX518177
                                                                                                                           Homo sapiens (human)
                                                                                                                                                        AX518177.1 GI:23567516
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                                                                   lominidae; Homo
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/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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  J (bases 1 to 24)
Saori, K., Akira, S. and Yasuhiro, F.
Gene RecQ5 encoding helicase
Patent: JP 1999276173-A 22 12-OCT-1999;
AGENE RES INSTI CO LTD
                                                                                                                  E30500 24
Gene RecQ5 encoding helicase.
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                                                                  unidentified
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E30500.1 GI:13021449
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Sequence 270 from Patent
CS064922
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                                                       unclassified.
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Patent: WO 2005031004-A 270 07-APR-2005;
                                                                                                                                                                                                                                                                                                                                                                          Snaidr, J., Beimfohr, C., Theler Method for the specific rapid
                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct synthetic construct
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Saccharomycetales; mitosporic
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:5476"
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Pred. No. 1.9e+05;
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Pred. No. 1e
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Shimamoto, A., K
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 Kitao, S.
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  and Furuichi, Y.
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OS Unidentified
PN 17 199276173-A/22
PD 12-OCT-1999
PF 27-MAR-1998 JP 1998081492
PF 27-MAR-1998 JP 1998081492
PR SAORI KITAO, AKIRA SHIMAMOTO, YASUHIRO FURUICHI PC C12N15/09, A01K67/027, C07K16/40, C12N5/10, C12N9/00, C12P21/02, PC C12P21/08, G10N33/50, G01N33/53, G01N33/577//(C12N15/09, C12R1:PC C12N15/10, C12R1:91), (C12P21/08, C12R1:91), C12N15/10, C12N15/10
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Shimamoto,A., Kitao,S. and Furuichi,Y.
Human gene RecQ4 encoding helicase
Patent: US 6335435-A 25 01-JAN-2002;
Location/Qualifiers
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(C12N15/00,C12R1:91), (C12N5/00,C12R1:91)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Location/Qualifiers
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RESULT 1
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AR019246/c
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1 (bases 1 to 22)
Bestwick, R.K. and Kellogg, J. Anne.
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AR019246
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Patent: US 5783393-A 7 21-JUL-1998;
Location/Qualifiers
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Kellogg, J. Anne. and
Plant tissue/stage
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                                                                                                   Raspberry promoters for expression of Patent: US 5783394-A 18 21-JUL-1998;
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Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing
disequilibrium map of the human genome
Patent: US 6537751-A 1662 25-MAR-2003;
Genset S.A.;;
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AR289927
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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 164831
; SEQ ID NO 164831
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-164831
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Keynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
CAPPLICANT: Marshall, William
APPLICANT: MARSHALL, William
APPLICANTON NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: MO/426,137
PRIOR APPLICATION DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOPTMARE: Proprietary
SEQ ID NO 164932
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Search completed: March Job time: 501.333 secs
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US-11-083-784-164932
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Publication No. US20050245475A1
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US-11-101-244-572442
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US-11-101-244-572442/c
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US-11-101-244-453541
            FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
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SEQ ID NO 453541
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SEQ ID NO 572442
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APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
APPLICANT: Leake, Devin
                                                                                                                                                                               APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
                                                                                                                                                                                                                                                                                         APPLICANT: Dharmacon, APPLICANT: Khvorova,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
FILING DATE: 2002-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ch 71.0%; Score 14.2; DB 10; 1 Similarity 84.2%; Pred. No. 7.2e+02; 16; Conservative 0; Mismatches 3:
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l Similarity 63.2%;
l2; Conservative
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Reynolds, Angela
                                                                                                                                                                                                                                                                                                                                                                           Application US/11083784
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Pred. No. 7.2e+02;
4; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
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; ORGANISM: Homo sapiens
US-11-083-784-164632
                                                                                                                                                                                                                                     US-11-083-784-164831
Sequence 164831, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/110/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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SOFTWARE: Proprietary
SEQ ID NO 164632
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Matches
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SOFTWARE: Proprietary
SEQ ID NO 164732
LENGTH: 19
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Publication No. US20050245475A1
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Best Local Similarity 63.2%;
Matches 12; Conservative
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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
                               FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
                                                                         APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
                                                                                                                                                                          APPLICANT: Dharmacon, Inc. APPLICANT: Khvorova, Anas APPLICANT: Reynolds, Ange
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PRIOR APPLICATION NUMBER: US/10/714,333 PRIOR FILING DATE: 2003-11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
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Scaringe, Stephen
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Sequence 289129, Application US/11101244

Publication No. US20050246794A1

PublicANT: INFORMATION:
APPLICANT: Chvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
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APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOTTWARE: Proprietary
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US-11-101-244-289129
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US-11-101-244-164932
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-164831
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US-11-101-244-164932
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SEQ ID NO 164831
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            CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
CURRENT FILING DATE: 60/502,050
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
APPLICANT: Leake, Devin
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NUMBER OF SEQ ID NOS: 1591911
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TYPE: RNA
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Local Similarity 63.2%;
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Similarity 63.2%;
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APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/50,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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; ORGANISM: Homo sapiens
US-11-101-244-289129
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APPLICANT: Dharmacon,
APPLICANT: Khvorova,
                                                                                                                                                                                                                                                                                                                Sequence 453541, Application US/11101244 Publication No. US20050246794A1
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SEQ ID NO 440211
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SOFTWARE: Proprietary
SEQ ID NO 289129
LENGTH: 19
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Matches 12; Conserv
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/426,137 PRIOR FILING DATE: 2002-11-14
WIMBER OF SEQ ID NOS: 1591911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: RNA
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Reynolds, Angela
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63.2%;
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84.2%; Pred. No. 7.
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Pred. No. 7.2e+02;
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US-11-101-244-164632
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TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1063031
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LENGTH: 61
TYPE: DNA
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
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Best Local Similarity
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PRIOR FILING DATE: 2004-10-08
PRIOR APPLICATION NUMBER: US 60/514,180
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 404
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirna
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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CURRENT FILING DATE: 2004-10-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
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les 15; Conserv
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Reynolds, Angela
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-164732
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US-11-101-244-164632
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APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anas
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Publication No. US20050246794A1
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Best Local Similarity 63.2%;
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Publication No. US20050246794A1
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                   APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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TYPE: RNA
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NUMBER OF SEQ ID NOS: 1591911
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Reynolds, Angela
Leake, Devin
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Reynolds, Angela
Leake, Devin
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Pred. No. 7.2e+02;
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Length 19;

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APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-559589
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                                                                                                                                                                                                                                                                              Sequence 559589, Application US/11083784 Publication No. US20050245475A1 GENERAL INFORMATION:
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Publication No. US20050246794A1
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PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: Patentin version 3.2
SEQ ID NO 21315
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Best Local (
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APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
APPLICANT: Leake, Devin
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CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR FILING DATE: 200426,137
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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APPLICANT: Khvorova, Anas
APPLICANT: Reynolds, Ange
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marchall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional
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Similarity 75.0%;
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Similarity 80.0%;
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; Pred. No. 4.7e
1; Mismatches
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Pred. No. 5.7e+02;
3; Mismatches 1;
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FILE REFERENCE: MMI1120-4
CURRENT APPLICATION NUMBER: US/10/972,767
CURRENT FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US 60/617,383
PRIOR FILING DATE: 2004-10-08
PRIOR APPLICATION NUMBER: US 60/514,180
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 404
SOFTWARE: PatentIn version 3.3
SEQ ID NO 351
LENGTH: 25
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US-10-972-767-351/c
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                                                                                                                                              Sequence 48, Application US/10972767
Publication No. US20060008815A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Proprietary
SEQ ID NO 559589
LENGTH: 19
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                                                            APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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Best Local :
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APPLICANT: DeNise, Sue
APPLICANT: Bates, Stephen
APPLICANT: Fantin, Dennis
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING CANINE BREEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fantin, Dennis
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING CANINE BREEDS
TITLE OF INVENTION: FOR GENETIC TRAITS AND VERIFYING PARENTAGE OF CANINE ANIMALS
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APPLICANT: Rosenfeld, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 25
TYPE: DNA
ORGANISM: Artificial sequence
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PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
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Local Similarity 75.0%;
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DeNise, Sue
Bates, Stephen
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                                                                          Hutton, Michelle
                                                                                            Rosenfeld, David
Kerr, Richard
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Pred. No. 6.2e+02;
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Pred. No. 5
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5.7e+02;
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FEATURE:

ORGANISM: Artificial

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; OTHER INFORMATION: Probe US-11-136-527-291020
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                                                                                                                      ; ORGANISM: homo sapien US-11-175-859-32149
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PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 291028
LENGTH: 25
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Best Local Similarity
Matches 17; Conserv
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CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32149
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-05
CURRENT FILING DATE: 2005-05-05-05
                                                                                                                                                                                                                                                                                                       APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
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                                                                                                                                         ORGANISM:
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85.0%;
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85.0%;
                                                                    75.0%; Score 15; DB 12; Length 50; 88.2%; Pred. No. 3.7e+02;
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Pred. No. 2
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Pred. No. 2.4e+02;
                                                     Mismatches
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 345949
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Publication No. US20060024715A1
GENERAL INFORMATION:
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Publication No. US20060024715A1
GENERAL INFORMATION:
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SEQ ID NO 4340
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Publication No. US20060003322A1
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Best Local (
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CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILLING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
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APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
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ORGANISM: Human
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66.7%;
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80.0%; Pred. No. 4.7e+02;
tive 1; Mismatches 3;
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US-11-121-849-113350
                                                                                                                                   US-11-136-527-290998
                                                                                                                                                      RESULT 6
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; ORGANISM: Homo sapien
US-11-121-849-284248
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US-11-121-849-284248
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Publication No. US20050272080A1
GENERAL INFORMATION:
                                                                          GENERAL INFORMATION:
                                                                                            Sequence 290998, Application US/11136527
Publication No. US20050287570A1
                                                                                                                                                                                                                                                                                        Matches
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CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 284248
                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                             Query Match
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded:
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                     APPLICANT: Wyeth APPLICANT: Mount
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression
FILE REFERENCE: 031896-041000 (AM101086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: John Palma TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded TITLE OF INVENTION: Microarrays FILE REFERENCE: 3684.1
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                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
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Similarity 94.1%;
16; Conservative
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85.0%;
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Pred. No. 2.4e+02;
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                 Profiling
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                   of Rat Genes
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APPLICANT: "Jein Milliam M TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AMIDIO86)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PRILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: PatentIn version 3.2

SEQ ID NO 291020

LENGTH: 25
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US-11-136-527-291020
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SEQ ID NO 291008
LENGTH: 25
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Publication No. US20050287570A1
GENERAL INFORMATION:
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APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
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CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
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Local Similarity 85.0%;
les 17; Conservation
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17; Conserv
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85.0%;
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Pred. No. 2.
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Pred. No. 2.4e+02;
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US-10-923-476A-363
; Sequence 363, Application US/10923476A
; Publication No. US20050288242A1
; Publication No. US20050288242A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: MCSwiggen, James
; TITLE OF INVENTION: RNA Interference Me;
; TITLE OF INVENTION: Short Interfering |
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US-10-923-476A-254/c
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                                                                                                                                     RESULT 2
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PRIOR FILING DATE: 2002-09-10
PRIOR PELICATION NUMBER: PCT/US02/16840
PRIOR PELING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2004-05-24
PRIOR PILING DATE: 2004-05-24
PRIOR PILING DATE: 2004-05-24
PRIOR APPLICATION NUMBER: US 10/826,966
PRIOR APPLICATION NUMBER: US 10/757,803
PRIOR FILING DATE: 2004-01-14
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Pat
SEQ ID NO 254
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TITLE OF INVENTION: RNA Interference Mediated Inhibition Of RAS Gene Expression Using
TITLE OF INVENTION: Short Interfering Nucleic Acid (siNA)
FILE REFERENCE: 400/231 (MBHB01-1158-B)
CURRENT APPLICATION NUMBER: US/10/923,476A
CURRENT FILING DATE: 2004-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT/US03/05346
PRIOR FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 10/720,448
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US 10/693,059
PRIOR FILING DATE: 2003-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 766
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96
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                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 19
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 RNA Interference Mediated Inhibition Of RAS Short Interfering Nucleic Acid (siNA)
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94.7%; Pred. No. 16;
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US-11-083-784-45882

US-11-083-784-355804

US-11-083-784-356702

US-11-083-784-559605

US-11-083-784-609758

US-11-083-784-609839
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45882, A
355584,
356702,
559605,
609758,
609839,
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 31
LENGTH: 33
TYPE: DNA
ORGANISM: Francisella tularensis
US-10-630-154-31
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US-10-630-154-31
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LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
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  Matches
              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                  APPLICANT: Anderson, Gary L
APPLICANT: Ott, Linda L
APPLICANT: Slezak, Thomas R
APPLICANT: Kuczmarski, Thomas R
APPLICANT: Vitalis, Elizabeth A
APPLICANT: Vitalis, Elizabeth A
TITLE OF INVENTION: Nucleotide Sequences Specific to Francisella Tularensis
TITLE OF INVENTION: Methods for Detection of Francisella Tularensis
FILE REFERENCE: IL-11031
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PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: PCT/US02/16840
PRIOR FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 400/231 (MBHB01-1158-B)
CURRENT APPLICATION NUMBER: US/10/923,476A
CURRENT FILING DATE: 2004-08-20
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SOFTWARE: PatentIn version 3.3
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PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US04/16390
PRIOR FILING DATE: 2004-05-24
                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/630,154
CURRENT FILING DATE: 2003-07-29
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: McCready, Paula M
APPLICANT: Radnedge, Lyndsey
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Local Similarity 73.7%;
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FILING DATE: 2003-10-23
APPLICATION NUMBER: US 10/444,853
FILING DATE: 2003-05-23
APPLICATION NUMBER: PCT/US03/05346
FILING DATE: 2003-02-20
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Anderson, Gary L
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Pred. No. 16;
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2: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO1_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq3:*
12: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq3:*
13: /cgn2_6/ptodata/1/pubpna/USI1_NEW_PUB.seq3:*
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         Sequence 164831, Sequence 289129, Sequence 164632, Sequence 572442, Sequence 164732, Sequence 164732, Sequence 164732, Sequence 164732, Sequence 1648311, Sequence 1648311, Sequence 1648311, Sequence 1648311, Sequence 1648311, Sequence 1648311, Sequence 106126, Sequence 106126, Sequence 106126, Sequence 106126, Sequence 1108127, Sequence 1108127, Sequence 138955, A Sequence 138956, A Sequence 138956, A Sequence 138956, A Sequence 1399516, Sequence 1399516, Sequence 1399516, Sequence 1070874, Se
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; ORGANISM: Probe Sequence
US-10-956-157-259791
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US-10-843-527-26645
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                                                   Sequence 26648, Application US/10843527
Publication No. US20050136395A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Bric Schell
TITLE OF INVENTION: Methods of Genetic Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 259791
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Best Local :
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LENGTH: 25
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Publication No. US20050136395A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods of Genetic Analysis of FILE REFERENCE: 3602.1
CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generat
FILE REFERENCE: 3602.1
CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
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APPLICANT: Eric Schell
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Pred. No. 1.4e+(
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                                                                       ; ORGANISM: SARS Virus
US-10-843-527-27622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: SARS Virus
US-10-843-527-27138
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                                                                                                                       PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence I
SEQ ID NO 27622
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                       Sequence 27622, Application US/10843527
Publication No. US20050136395A1
GENERAL INFORMATION:
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 27138
Query Match 71.0%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local :
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LENGTH: 25
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Publication No. US20050136395A1
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CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
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                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus FILE REFERENCE: 3602.1
                                                                                                                                                                                                                                                                                                        APPLICANT: Michael Mittmann APPLICANT: Eric Schell
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PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
                                                                                                            TYPE: DNA
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84.2%;
                                                                                                                                                          Sequence Listing Generator V 1.1
 Score 14.2; DB 9;
Pred. No. 1.4e+04;
0; Mismatches 3
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Pred. No. 1.4e+04;
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Pred. No. 1.4e+04;
0; Mismatches 3;
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RESULT 20 US-10-719-956-403149 밁

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; ORGANISM: Rattus norvegicus
US-10-719-956-403149
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US-10-719-900-613240/c
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US-10-719-900-559116/c
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CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 403149
LENGTH: 25
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Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 559116, Application US/10719900 Publication No. US20050026164A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 559116 LENGTH: 25
                                                                                                              Sequence 613240, Application US/10719900 Publication No. US20050026164A1 GENERAL INFORMATION:
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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l Similarity 84.2%;
l6; Conservative
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84.2%;
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Pred. No. 1.4e+04;
0; Mismatches 3;
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Pred. No. 1
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APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITTITE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 259790
US-10-956-157-259790
US-10-956-157-259790
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APPLICANT: Wounts, William
APPLICANT: MOUNTS, WILLIAM
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WIT TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
SEQ ID NO 227840
LENGTH: 25
TYPE: DNA
ORGANISM: Probe Sequence
US-10-956-157-227840
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                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 259790, Application US/10956157; Publication No. US20050118625A1; GENERAL INFORMATION:
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Publication No. US20050118625A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 613240
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Best Local Similarity
Matches 16; Conserva
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Best Local S
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TYPE: DNA
ORGANISM: Mus musculus
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2 TAAAAAGCTTCTTCAACAC 20
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84.2%;
                                                     71.0%; Score 14.2; DB 9;
84.2%; Pred. No. 1.4e+04;
tive 0; Mismatches 3;
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Pred. No. 1.4e+04;
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Pred. No. 1.4e+04;
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                                                                                                                                                                                                                                    Sequence 6, Application US/10640968A
Publication No. US20040224414A1
GENERAL INFORMATION:
APPLICANT: Julien, Bryan
TITLE OF INVENTION: TRANSPOSON-BASED TRANSFORMATION SYSTEM
FILE REFERENCE: 300622009800
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Matches
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Publication No. US20050214823A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 681188
LENGTH: 25
TYPE: NUMBER OF SEQ 1818
                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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                                                                                                                                                             CURRENT FILING DATE: 2003-08-13
PRIOR APPLICATION NUMBER: US 60/403,290
PRIOR FILING DATE: 2002-08-13
                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/640,968A CURRENT FILING DATE: 2003-08-13
                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 991174
             OTHER INFORMATION: Synthetic Construct
                                ORGANISM: Artificial Sequence FEATURE:
                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                        LENGTH: 33
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93.8%;
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Pred. No. 1.
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Pred. No. 1.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Receptor
FILE REFERENCE: 674580-2004
CURRENT APPLICATION NUMBER: US/10/714,161
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: PCT/GB02/02304
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: GB 0111959.3
PRIOR APPLICATION NUMBER: US 60/292,141
PRIOR APPLICATION NUMBER: US 60/292,141
PRIOR FILING DATE: 2001-05-18
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Publication No. US20040146910A1
GENERAL INFORMATION:
                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                              SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 79762
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
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Best Local
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Best Local :
                                                                                                                                                                                                                                               APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
CURRENT FILING DATE: 2003-11-20
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
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APPLICANT: Aparicio, San
APPLICANT: Dixon, John
                                                                                                                 TYPE: DNA ORGANISM: Rattus norvegicus
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ORGANISM: Artificial Sequence
                                                                                                                                              LENGTH:
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 2 TAAAAAGCTTCTTCAACAC 20
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84.2%;
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                                              Score 14.2; DB 7;
Pred. No. 1.4e+04;
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Pred. No. 1.
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Pred. No. 1.2e+04;
                                Mismatches
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; ORGANISM: Artificial Sequence; FEATURE:
; OTHER IMPORMATION: Oligonucleotide
US-10-220-481-169

Length 33

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Sequence 118837, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
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US-10-098-263B-118837
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                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118838
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 118837
LENGTH: 25
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Best Local Similarity
Matches 17; Conserv
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 118838
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Best Local (
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                                                                                    Query Match
                                                                                                                                                                                                                          APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
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                                                                        Local Similarity
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AAAAAGCTTCTGCAAGAC
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88.9%;
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85.0%;
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19
                                                                      Score 14.8;
Pred. No. 7.
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Pred. No. 7.
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RESULT 13

FILE REFERENCE: 3527.1

of Genetic Analysis of Rat

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TYPE: DNA
ORGANISM: Mus musculus
US-11-036-317-859238
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                                                                                              RESULT 15
US-10-719-956-681188
                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; Hamster sp. US-10-339-767-9
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US-10-339-767-9
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Sequence 681188, Application US/10719956
Publication No. US20040146910A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GMP Endotherapeutics, Inc.
APPLICANT: Taylor-Fishwick, David A
APPLICANT: Vinik, Aaron I
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Publication No. US20050214823A1
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.2 SEQ ID NO 9
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PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Assay for the Detection of Factors that Modulate the Expression TITLE OF INVENTION: of INGAP FILE REFERENCE: 9061X#L$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing
FILE REFERENCE: 3654.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/388,315
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/361,073
PRIOR FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/346,898 PRIOR FILING DATE: 2002-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/339,767
CURRENT FILING DATE: 2003-01-09
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 22
                                                                                                                                                                                                                                                                    / Match 72.0%;
Local Similarity 93.8%;
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Local Similarity 88.9%;
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Pred. No. 1.1e+04;
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RESULT 8
US-10-956-157-227426/c
; Sequence 227426, Application US/10956157
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                                                                                                                                                                                                   ; ORGANISM: Rattus norvegicus US-10-719-956-79761
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US-10-719-956-79761/c
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Best Local (
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 607427,836
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 72761
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 79761, Application US/10719956 Publication No. US20040146910A1 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 20
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CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2003-11-20
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Methods of Genetic Analysis of Rat FILE REFERENCE: 3527.1
CURRENT APPLICATION NUMBER: US/10/719,956
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xue Mei Zhou
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APPLICANT: Kemneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
FILE REFERENCE: PTS-0022
                                                                                                                                                                                                                               TYPE: DNA
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Conservative 0;
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No. 2.7e+03;
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CURRENT APPLICATION NUMBER: US/10/220,481
CURRENT FILING DATE: 2003-05-05
FRIOR APPLICATION NUMBER: PCT/IB01/00452
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 633
SOFTWARE: SegWin99, version 1.02
SEQ ID NO 169
LENGTH: 33
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US-10-220-481-169
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US-11-036-317-964784
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SEQ ID NO 227426
LENGTH: 25
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                                                                                                                                                              APPLICANT: ARICO, Maria B., et al.
TITLE OF INVENTION: Heterologous Expression of Neisserial Proteins
FILE REFERENCE: CHIR-15883/01US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. US20050118625A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED
TITLE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FAPLICATION NUMBER: US/10/956,157
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FLILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
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ORGANISM: Probe Sequence
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Pred. No. 5e+03;
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FILE APPLICATION UMBER: US/10/653,528
CURRENT EPILING DATE: 2003-09-02
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 32
LENGTH: 20
TYPE: "NOTE: THE TIME TO THE TIME THE TIME
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Sequence 32, Application US/10173192
Publication No. US20030236204A1
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
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US-10-653-528-32
; Sequence 32, Application US/10653528
; Publication No. US20040077578A1
; GENERAL INFORMATION:
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-192-32
US-10-13-192-43

; Sequence 43, Application US/10173192

; Publication No. US20030236204A1
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Best Local S
Matches 20
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CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 32
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TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
FILE REFERENCE: PTS-0022
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TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Local Similarity 100.0%;
nes 20; Conservative (
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US-10-371-962-10
US-10-665-971-10
US-10-637-759-10
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Pred. No.
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Pred. No. 33;
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US-10-173-192-67/c
Sequence 67, Application US/10173192
Publication No. US20030236204A1
GENERAL INFORMATION:
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; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-192-43
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NUMBER OF SEQ ID NOS: 71
SEQ ID NO 43
SEQ ID NO 43
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                               APPLICANT: Brett P. Monia
APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
TILE REFERENCE: PTS-002
CURRENT FILING DATE: 2003-09-02
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/10/173,192
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 43
LENGTH: 20
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Matches
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APPLICANT: Kenneth W. Dobie
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: ANTISENSE MODULATION OF HISTONE DEACETYLASE 2
FILE REFERENCE: PTS-0022
CURRENT FILLYS DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 71
LENGTH: 20
TYPE: DNA
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Best Local 9
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Publication No. US20040077578A1
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APPLICANT: Kenneth W. Dobie
TITLE OF RIVENTION ANTISENSE MODULATION OF HISTONE DEACETYLASE 2 EXPRESSION
FILE REFERENCE: PTS-0022
CURRENT APPLICATION NUMBER: US/10/173,192
CURRENT FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: H. sapiens
                                   TYPE: DNA ORGANISM: Artificial Sequence
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OTHER INFORMATION: Antisense Oligonucleotide
                  FEATURE:
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